

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 126 100

TO: Ginny Portner

Location: REM/3B02/3C18

Art Unit: 1645

Tuesday, July 06, 2004

Case Serial Number: 09/732091

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

### Search Notes

Dear Examiner Portner,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



### STIC-Biotech/ChemLib

196106

From:

Portner, Ginny

Sent:

Tuesday, June 29, 2004 6:07 PM

To:

STIC-Biotech/ChemLib

Subject:

RE: 09/732,091

try 09/732,091

Ginny Rortner Remsen Building Art Unit 1645 Room E03, B02 (571) 272-0862

----Original Message-----

From:

STIC-Biotech/ChemLib

Sent:

Tuesday, June 29, 2004 4:23 PM

To:

Portner, Ginny

Subject:

RE: 09/732,081

There is no valid CRF for this Serial Number. Please provide us with another Serial Number from the Parent Application.

LEONARD 22520

----Original Message----

Portner, Ginny From: Sent:

Tuesday, June 29, 2004 4:21 PM

To:

STIC-Biotech/ChemLib Subject: 09/732,081

Importance:

Please search SEQ ID NO 3 and 4 with respect to polypeptides/proteins. The nucleic acid should be back translated to the polypeptide. Thanks.

Ginny Bortner Remsen Building Art Unit 1645 Room E03, B02 (571) 272-0862

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (w	here applic.)
STN:	
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Query Match Best Local

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disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
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; Pred. No. 1.9e-118;
0; Mismatches 0;
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N-PSDB; AAT67811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                 1 MAXKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                               Length 253;
                                                            ; DB 5; ; 1.8e-118;
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Pred. No. 1.
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                                                           100.0%;
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Helicobacter sp. HP30 protein
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N-PSDB; AAD44535.
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AAE26878;

RESULT 2 AAE26878 Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.

The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a

Disclosure; Page 122-123; 127pp; English.

Tian J,

Novel  $^{\mathsf{the}}$ 

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The present sequence is a H. pylori cytoplasmic protein. The protein may identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 mucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest;
                                                                                                                                                                                                                                                                                                                                    particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
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Pred. No. 1.4e-117;
1; Mismatches 1;
61; Page 651; 1481pp; English
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Best Local Similarity 99.2
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AAW24673 standard; protein; 253 AA AAW24673; 

AAW24673 RESULT

(first entry) 12-AUG-1997

H. pylori cytoplasmic protein, 4095342.aa.

Transmembrane, cytoplasmic; cell envelope, flagella, transport, secreted, periplasmic, chronic gastritis, duodenal ulcer disease; activator, inhibitor; bacterial life cycle, vaccine, immunise, detection, antisense, inhibition.

Helicobacter pylori

WO9719098-A1

29-MAY-1997

96WO-US018542 15-NOV-1996; 95US-00561469 17-NOV-1995;

(ASTR ) ASTRA

Smith DH;

WPI; 1997-298052/27

N-PSDB; AAT77491

Helicobacter pylori nucleic acid sequences and related proteins - used for diagnostics and therapeutics.

Claim 18; Page 184; 235pp; English

This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA creaments were blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate to pwritied DNA samples were then sequenced. Note: The ORF/protein reference number for this sequence was obtained from the related specification, WO9640893

Sequence 253 AA;

ö 240 120 120 181 GRGLSLAGNOVLTRILSFLIGPVGWIIIGVWTAIDIAGPAYRVTIPACIVVATLRIKTQQ 240 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180 LEEMDDEEVKEMCDELSIKNTDNINROALSAATITIERGGGFKSYOLAVIVANAVAKTIL 180 9 09 IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER MAYKYORDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ Gaps 0; Score 1270; DB 2; Length 253; Pred. No. 1.4e-117; 1; Mismatches 1; Indels ( 99.3%; Query Match Best Local Similarity 99.2 Matches 251; Conservative 61 61 121 121 181

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241 ANGDKKSLQIESI 253 ANEDKKSLQIESV 241

RESULT 5 AAW20866

AAW20866 standard; protein; 256 AA.

AAW20866;

18-JUL-1997 (first entry)

H. pylori cytoplasmic protein, 12ge20305orf30.

Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis 

Helicobacter pylori

WO9640893-A1

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The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for by computer evaluation. To identify likely H. pylori antigens for vaccine by computer, the amino acid sequences predicted room various ORF were analysed for significant homology to other known or exported membrane analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.

Claim 61; Page 651; 1481pp; English.

Mellgaerd BL;

OT,

D, Berglindh

Smith

(ASTR ) ASTRA AB.

WPI; 1997-052306/05. N-PSDB; AAT67811.

95US-00487032.

07-JUN-1995; 01-APR-1996;

TTGGATTTGTTTGAGGTGCTTGTTTTTGGTAAGACGGCGAAAAAAGACACAATGAAAAA 120 CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 180 240 300 100 420 140 9 80 1 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC TTGGAAGAAATGGATGAAGAAGTGAAGAAATGTGCGATGAATTATCCATAAAAAC 4400 Length:
Matches:
Conservative:
Mismatches: Indel8: US-09-732-091-3 (1-759) x AAW20486 (1-253) 6.94e-134 1270.00 99.60% 99.21% 94.14% Best Local Similarity: Query Match: Percent Similarity: 19 61 361 ' 121 41 181 241 à 셤 ò g à 셤 g ð ò P q à à 유

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421 ACGGACAATTTAAACAGACCATTAAGGCGCGGCGACTTTAACGTGTTTTAAAATGGGG

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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori

WO9640893-A1 19-DEC-1996 06-JUN-1996;

H. pylori cytoplasmic protein, 4095342.aa.

(first entry)

29-JUL-1997

AAW20486;

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AAW20486 standard; protein;

RESULT 3 RESULT

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5: /cgn2_6/ptodate/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodate/2/pubpaa/US08_NBM_PUB_PEP:*
7: /cgn2_6/ptodate/2/pubpaa/US08_NBM_PUB_PEP:*
8: /cgn2_6/ptodate/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodate/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodate/2/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodate/2/pubpaa/US09_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1276540 seqs, 311283816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
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/cgn2_6/1
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                                                                                                                                                                          July
                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB.seq
Maximum DB seq
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                                                                                                                CM protein
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                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli	Sequence 9162, Ap	Sequence 9163, Ap	Sequence 3164, Ap	Sequence 7699, Ap	Sequence 7698, Ap	Sequence 414, App	Segmence 20, Appl	Seguence 17, Appl	Seguence 19, Appl	Sequence 18, Appl	Seguence 16, Appl	Sequence 43832, A	Sequence 191043,
SUMMARIES	US-09-732-091-4 IIS-09-732-091-44	US-10-335-977-9162	US-10-335-977-9163	JS-10-335-977-9164	US-10-335-977-7699	US-10-335-977-7698	US-09-882-227-414	US-09-732-091-20	US-09-732-091-17	US-C9-732-091-19	US-09-732-091-18	US-09-732-091-16	US-10-282-122A-43832	US-10-437-963-191043
DB	on o	12	12	12	12	12	10	σ	σ,	σ	σ	Φ	12	16
f Query Match Length DB	253	253	253	256	248	237	155	49	38	41	0.6	GE.	1009	815
% Query Match	100.0	99.3	99.3	99.3	56.5	56.0	36.9	19.7	15.5	15.2	11.9	11.7	7.7	7.5
Score	1279	1270	1270	1270	722	716	472.5	252	198	194	152	150	98.5	97.5
Result No.	но	m	4	ស	9	r~	œ	6	10	11	12	13	14	15

Sequence 76490, A Sequence 42, Appl Sequence 7400, Ap Sequence 1435, A Sequence 54543, A	Sequence 29, Appl Sequence 169, App Sequence 220, App Sequence 230, App	Sequence 52737, A Sequence 47217, A Sequence 5229, Ap Sequence 5251, Ap	4	Sequence 107, App Sequence 43207, A Sequence 122554, Sequence 590, App Sequence 590, App Sequence 7664, App	749', 50', 7 58561 60', 7 19942 4, Apr
12 US-10-282-122A-76490 15 US-10-369-493-42 14 US-10-032-585-7400 14 US-10-156-761-14395 12 US-10-282-122A-54543	9 US-09-919-172-29 14 US-10-205-219-169 15 US-10-341-434-220 15 US-10-341-434-230	12 US-10-282-122A-52737 12 US-10-282-122A-47217 15 US-10-369-493-5229 9 US-09-815-242-5251	16 US-10-813-744-1241 16 US-10-412-693B-682 17 US-10-412-693B-682 18 US-10-369-493-1075 19 US-10-444-599-222059	12 US-10-422-024-107) 12 US-10-425-114-42207 16 US-10-437-963-122954 12 US-10-231-278-590 15 US-10-291-172-590 14 US-10-032-585-7664	, p
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## ALIGNMENTS

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121 LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTIL 180
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                                                                    APPLICANT: Tian, Jing-Hui
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
TITLE OF INVENTION: Holiobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REPERBUCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1279; DB 9; Length 253; Best Local Similarity 100.0%; Pred. No. 4.8e-115; Matches 253; Conservative 0; Mismatches 0; Indels 0.
              Sequence 4, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Helicobacter sp.
                                                                                                                                                                                                                                                                                               253
US-09-732-091-4
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IAEELQYYGSNSFASFIKGEGYLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ
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Publication No. US20040052799A1
GENERAL INFORMATION: WITH et al
APPLICANT: DOUGLAS SMITH et al
IITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: PRIATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%; Score 1270; DB 12;
99.2%; Pred. No. 3.6e-114;
tive 1; Mismatches 1;
                                                                                                                                                 APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY, AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEC ID NO: 9462:
SEQUENCE CHARACTERISTICS:
                                                                                   APPLICATION NUMBER: US/10/335,977 FILING DATE: 30-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...253; SEQUENCE DESCRIPTION: SEQ ID NO: 9162: US-10-335-977-9162
COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              & COCKFIELD
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TYPE: amino acid
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STREET: 28 State Street
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STATE: Massachusetts
COUNTRY: USA
                                                              CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS
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Best Local Similarity 99.2
Matches 251; Conservative
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GRGLSLAGNQVITRTLSFLTGPVGWIITGWWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               APPLICANT: Tian, Jing-Eui
APPLICANT: Tian, Jing-Eui
APPLICANT: Malker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REPRENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT APPLING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SCFTWARE: Patentin Ver. 2.1
LENGTH: 265
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 265;
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100.0%; Pred. No. 5.1e-115;
iive 0; Mismatches 0;
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ZIF: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9162, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:
                                                                                                                                                                                   RESULT 2
US-09-732-091-44
IS-09-64, Application US/09732091
Parent No. US20020167368A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
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                                                                                                                     241 ANGDKKSLQIESI 253
                                                                       ANGDKKSLQIESI 253
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Best Local Similarity 100.
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
, ORGANISM: Helicobacter sp.
US-09-732-091-44
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61 IABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1270; DB 12;
Pred. No. 3.6e-114;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
RAME: MANDEAGOURAS, AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECHMUNICATION INFORMATION:
TELEPAX: (617)742-4214
                                                                                                                                                                                                              APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMB/XEY: misc feature
LOCATION: (B) LÖCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 9164:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT
                         ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 256 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 9164:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 ANEDKKSLOIBSV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ANGDKKSLOIESI 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 251; Conservative
                                                                                                                                                               SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-335-977-9164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-335-977-7699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LEEMDDEBVXEMCDELSIKNYDNLNRQALSAATLTLFKNGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGLSLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IABELQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTBTTLIEQNMLSKILERS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LEEMDDEBVXEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GRGLSLAGNOVLTRILSFLIGPVGWIIIGVWTAIDIAGPAYRVTIPACIVVATLRIKTQQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDJYAKYAER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.3%; Score 1270; DB 12; Best Local Similarity 99.2%; Pred. No. 3.6e-114; Matches 251; Conservative 1; Mismatches 1;
           MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBW PC Compatible
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34/993,002
FILING DATE: 17-DEC-197
ATTORNEY/AGENT INFORMATION:
NAME: MANCHAGOLIA AMY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ. ID NO: 9163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...253
SEQUENCE DESCRIPTION: SEQ ID NO: 9163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9164, Application US/10335977
Publication No. US20040052799Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10031
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ANGDKKSLQIESI 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
APPLICANT: Tomb, Jean-Francois
APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGNSFANFFRDEGVLYKEILCDACDHLDINYNERSATSLIEGNMLSKLLKDSLEKMSGRE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 GSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDEE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 VKEMCDELSIKNTDNL---NRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGL- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LEFLKRISSSDLKDLFDALVYDEDGTLRWNBELTSLTEYQRYGHDYAKYPRRIAEELQRY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LEFLKQLESSDLLDJFEVLVFGKDGEKRHNEKLJSSIEYKRHGDDYAKYAERIAEELQYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 SLAGNQVLTRTLSFLTGPVGKIITGVWTAIDIAGPAYRVTIPACIVVATLKK 237
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                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-197
ATTORNEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 35,207
REFERENCE/DOCKET NUMBER: GTM-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)722-7400
TELEPRAK: (617)742-7414
INFORMATION FOR SEQ ID NO: 7698:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...237
SEQUENCE DESCRIPTION: SEQ ID NO: 7698:
                                                                                          COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Helicobacter pylori
                    ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 414, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                FILING DATE: 30-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-10-335-977-7698
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US-09-882-227-414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 EVKEMCDELSIKNTDNL---NRQALSAATLILFKMGGFKSYQLAVIVANAVAKTILGRGL 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 -SLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLKLK 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.3%; Pred. No. 2.8e-61;
Matches 141; Conservative 36; Mismatches 53; Indels
                                                                                                                                                                                         SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...248
; SEQUENCE DESCRIPTION: SEQ ID NO: 7699:
US-10-335-977-7699
                                                                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM EC COMpatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GTN-018
TELEPONAUNICATION INFORMATION:
TELEPHONE: (617) 727-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 7699:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7698, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-335-977-7698
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Length 38;

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Sequence 19, Application US/09732091
Fatent No. US200201073681
GENERAL INFORMATION
APPLICANT: Halker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Halver, Richard I.
APPLICANT: Halver, Richard I.
APPLICANT: Halver, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANTON: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
CURRENT APPLICATION: Horreof
CURRENT APPLICATION: NUMBER: US/09/732,091
CURRENT PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09732091
Patent No. US20020107368A1
GENERAL INFORMATION
APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TITLE OF INVENTION: thereof
FILE REFERENCE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 NRQALSAATLTLFKMGGFXSYQLAVIVANAVAKTILGRGLS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NRQALSAATLTLFKWGGFKSYQLAVIVANAVAKTILGRGLS 41
                                                                                                                                                                                                                              1 DYAKYABRIABELQYYGSNGFASFIKGEGVLYKEILCD 38
                                                                                                                                                                                                53 DYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCD 90
                                                                                                 Query Match 15.5%; Score 198; DB 9; I
Best Local Similarity 100.0%; Pred. No. 7.9e-12;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 15.2%; Score 194; DB 9; 1
l Similarity 100.0%; Pred. No. 2.1e-11;
41; Conservative 0; Mismatches 0;
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                           ORGANISM: Helicobacter sp. US-09-732-091-17
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CRGANISM: Helicobacter sp.
US-09-732-091-18
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Best Local Similarity
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Best Local Similarity
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US-09-732-091-18
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LENGTH: 41
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SEQ ID NO 18
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       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                          98 NYNKKTETTLIEGNMISKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL 154
                                                                                                                                                                                                                                                                                                                38 NEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV 97
                                                                                                                                                                                                                                                                                                                                      2 NBDLTNSTEYKRYGHDYAKYPRIAEELQHYGGNSFANFFRDEGLYKEILCDACDHIKV 61
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Sequence 20, Application US/09732091

Patent No US20020107368A1

APPLICANT: Title No Usable Sequences and uses

TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses

TITLE OF INVENTION: Helicobacter proteins, gene sequences

TITLE OF INVENTION: Helicobacter proteins, gene sequences

CURRENT APPLICATION NUMBER: US/09/732,091

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ. ID NOS: 44

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO
                                                                                                                                                                                                                                                                   3; Gaps
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APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
FILE REPERRECE: 7969-088
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
LENGTH: 38
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                                                                                                                                                                                                                 36.9%; Score 472.5; DB 10; Length 155; 63.3%; Pred. No. 1.8e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQIE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 49;
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100.0%; Pred. No. 6.9
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TLFKAGGSHSYALAVSVADAWRQTLG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 TLFKMGGFKSYQLAVIVANAVAKTILG 181
PRICE FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 414
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Patent No. US20020107368A1
GENERAL INFORMATION:
                                                                                         LENGTH: 155
TYPE: PRT
CRGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                93; Conservative
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PORGANISM: Helicobacter sp.
US-09-732-091-20
                                                                                                                                                                                                                                  Best_Local Similarity
Matches 93, Conserv
                                                                                                                                                                  US-09-882-227-414
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US-09-732-091-20
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US-09-732-091-17
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Gaps

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Length 41;

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Length 30 Indels 16;

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated Wit
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (51221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
LENGTH: 815
                                                                                                                                                                                                                                                                                                                             708 YNNDLELNEQSIEMEMSKLNLTDDNDINEILAWRGEQEE-----LEOKR--DTYKK 756
                                                                                                                                                                                                                                                                                                                                                                                   57 YAERIABELQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKKTE--TTLIE---- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                 757 RYHEFEMEIA-----RLESLTKD-----KBLLDS--DKLKDEYEQKKEKMNTLIDEYSAV 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       805 HYQCQNNINKTQSIVSHINYLMQBLKDQQBIFQLABIYSGKNNKNLTLENFVLIYYLDQI 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSAATLITLFKWGGFKSYQLAVIVANAVAKTILGRGLS-----LAGNQVLTRTLSFLT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 IAQANIRLATMSD-NRYQL-----IRREAVSHGLSGLEIDVFDLHSNK--SRHISSLS 914
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                                                                                                                                                                                                                                                                               5 YDRDLBP-----LKQLESSDLLDLFEVLVFGXDGEKRHNEKLTSSIEYKRHGDDYAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLN-----
                                                                                                                                                                      7.7%; Score 98.5; DB 12; Length 1009; 22.5%; Pred. No. 3.2; ive 45; Mismatches 83; Indels 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INPORMATION: Clone ID: PAT_MRT4530_8739C.1.pep
US-10-437-963-191043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 191043, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                           CRGANISM: Staphylococcus aureus
US-10-282-122A-43832
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                      Query Match
Best Local Similarity 22.5*
Matches 66; Conservative
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ORGANISM: Oryza sativa
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                  SEQ ID NO 43832
LENGTH: 1009
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IITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tian, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Jackson, W. James
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFG 30
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CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/732, D91
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43832, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PRIICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-03-21
                                             Sequence 16, Application US/09732091
Patent No. US200230107368A1
GENERAL INFORMATION:
APPLICANT: Tian, Jing-Hui
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Helicobacter sp. US-09-732-091-16
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                                                                                                                                                                                                                                                    FILE REFERENCE:
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635 RELEALVKOLCMISSARKALEADLDEATKSLDEMNRSALS 674

Search completed: July 5, 2004, 03:13:58 Job time : 34 secs

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Skelton, J.; Stevens, Salmonella enterica se
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              Wature 413, 848-852, 2001

Wature 512, 2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-237 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33434,1; PID:g13359467; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%; Score 265; DB 2; Length 23 32.6%; Pred. No. 1.4e-12; ive 40; Mismatches 101; Indels
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Best Local Similarity 32.6
Matches 79; Conservative
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Best Local Similarity 30.8
Matches 76; Conservative
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Dypotherical protein b0011 - Escherichia coli (strain K-12)

C'Species: Escherichia coli

C'Species: Escherichia coli

C'Species: Escherichia coli

C'Species: 12-68p-1997 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002

C'SAccession: C64721; D56689; S28462

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997

A;Flitle: The complete genome sequence of Escherichia coli K-12.

A;Recence unmber: A64720; MUID:97426617; FMID:9278503

A;Accession: C64721

A;Status: nucleic acid sequence not shown; translation not shown

A;Residues: 1-237 *cBLAT>

A;Cross-references: GB:AE000112; GB:U00096; NID:91786192; PIDN:AAC73122.1; PID:g1786193;

A;Cross-references: GB:AE000112; GB:U00096; NID:91786192; PIDN:AAC73122.1; PID:g1786193;

A;Accession: D56688

A;Accession: D56
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3 YKYDRDLEFLKQLESSDLIDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE
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C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C.Accession: AE0360
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Bougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gispedies: Staphylococcus aureus
Cispedies: Staphylococcus aureus
Cispedies: Staphylococcus aureus
Cispedies: Staphylococcus aureus
Cispedies: C69910
Cisped
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A;Cross-references: GB:BA000018; PID:g13701144; PIDN:BAB42439.1; GSPDB;GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805 HYQCQNNINKTQSIVSHINYINQELKDQQEIFQLAEIVSGKNNKNLTLENFVLIYYLDQI 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-282 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92208.1; PID:g15980920; GSFDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 YAERIAEELQYYGSNSPASFIKGEGVLYKEILCDVCDKLKVNYNKKTE--TTLIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 YDRDLEF-----LKQLESSDLLDLFEVLVPGKDGEKRHNEKLTSSIEYKRHGDDYAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0360
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YPO2963 [imported] - Yersinia pestis (strain CO92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SA1181 [imported] - Staphylococcus aureus
          Length 39
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                                                                                                                                                                                                                                                                I MAYRYDSDLEFIKRLSSSDLKDLFDALVYDEDGTLRMNE 39
     Score 133; DB 2; L
Pred. No. 0.00096;
5; Mismatches 8;
                                                                                                                                                                                                                 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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          10.4%;
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                                                                                                             Conservative
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                                                              Similarity
26; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SA1181
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     Query Match
Best Local &
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C;Species: Helicobacter pylori
C;Species: Helicopacter pylori
C;Species: Helicopacter pylori
C;Species: Helicopacter B; Helicopacter B; Helicopacter B; Helicopacter pylori
C;Species: He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Escherichia coli

C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C.Date: 16-Feb-2001

C.Date: 16-Feb-2001

A.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A.Fitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A.Facession: C85481

A.Facession: C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrain
                                                                    60 RIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIECNMLSKILER 119
169 VIVANAVAKTILGRGLSLAGNQVLTRTLSFLFGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIAGELQHFGGDSIANKLRGHGKLYRAILLDVSKRLKLKADKEMSTFEIEQQLLEQFLRN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----HLLSSOLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIVANAVAKTILGRGLSLAGNOVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YKYDRDLEFLKQLESSDILDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLNDSDLDFLQHCSEEQLANFARLLTHNEKGKTRLSSVLMRNELFKSMEGHPEQHRRNWQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.5%; Score 262; DB 2; Length 237; 30.8%; Pred. No. 2.3e-12; ive 45; Mismatches 90; Indels

    Escherichia coli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable oxidoreductase Z0011 [imported]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 30.84
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                    223 LQIACLR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 IVVATLR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQIACLR 229
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16

756 109

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A,Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A,Reference number: A81250; MUID:20150912; PMID:10688204
A,Accession: CB1380
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-311 cPAR>
A,Crossreferences: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74209.1; PID:g69676enetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: July
Job time : 14 secs
          Nature 403, 665-668,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Cj0411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254
                                                                                                                                                                                                                      A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Mycoplasma pulmonis
Cispecies: Mycoplasma pulmonis
Cipate: 24-May-2001 #text_change 03-Aug-2001
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
Cipate: 24-May-2001 #sequence_revision 2001
Cipate: 24-May-2001 #sequence 0f the murine respiratory pathogen Mycoplasma pulmay A; Reference number: A99512; MUID:21267165; EMID:11353084
A; Accession: G90546
A; Accession: G90546
A; Accession: G90546
A; Accession: G90546
A; Residues: 1-1099 cxure
A; Residues: 1-1099 cxure
A; Residues: 1-1099 cxure
A; Residues: 1-1099 cxure
A; Experimental source: strain UAB CTIP
A; Genetics:
C; Genetics:
A; Genetic code: SGC3
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C;Date: 24-May_2001 #sequence_revision 24-May_2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                             76 FIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSL-----EEMDDEE 128
                                                                                                                                                                                                                                                           FIKMS--LIKDQFISEVTRYSSDITAKVNTGEITTETAIKLLDKELSDIRNQDESMTRER 110
                                                                                                                                                                                                                                                                                                              129 VKE-MCDELSIKNTDNLNRQALSAATLTLFKMG-GFKSYQLAVI----VANAVAKTILGR 182
                                                                                                                                                                                                                                                                                                                                               111 VKQAVIIKASVXENNNVERNEV----INLVFAGVGFVTAGLQIVAGVGWVGSVVGSIPGT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||:
54 FHNDLKIFEGSLKNIAGKDGQNLYEIVIDKEQMKKHKNEIVEKETNEVYNEFFIDPKTKK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 RİBYKKR----KKMIGTKEYILEINNSDPEKEYFOPOKTSYDSGLVDIPLFYYNNKNSQT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 YNKKT-----ETTLIEGNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNINRQALS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 CNOKITQVNKSSQEKTNKELNMKSSSITKEINQSAESKTTSQNQDLSLNEQNNLNQSSVT 229
                                                                                                                                                                                            ---NSIASK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLTS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 SIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDV-----CDKLKVN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 A----ATLILF-KMGGFKSYQLAVIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQNTFEALSSSENQMPNEDISQTS-----SPARNQNLSQTNEVTPSFV 276
                                                                                                                                         19 DILDLFEVLVFGXDGEK-RHNEKLTSSIEYKRHGD-DYAKYAERIAEELQYYGSNSFAS-
                                                                                                                                                                                                                                                                                                                                                                                                                           :99
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                                                                   Length 282;
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                                                                                                                                                                                     EVLDAVERNPYSNSEDKTRORNNVMRSIMYNKONELDOVK----
                                                                                                           87;
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                                                                 DB 2;
4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.7%; Score 98; DB 2;
22.2%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                   183 GLSLAG-NQVLTRTLSFL---~-TGPVGWIITGV--
                                                               ; Score 98; DB;
; Pred. No. 4.9;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches
                                                             ch
1 Similarity 24.7%;
58; Conservative 34
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                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 53; Conserv
C;Genetics:
A;Gene: YP02963
                                                                                                      Matches
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A;Cross-references: GB:AL139075; GB:AL11168; NID:g6967817; PIDN:CAB74247.1; FID:g696: A;Bxperimental source: serotype O2, strain NCTC 11168
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 KFLIVLTKADLLSKKDLEEVIVYTKESLKSRLVDLDENLVEKIDFLCVSAKMASDFYKGL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 ASK--ESLÖKSGMOEF-----ENYLFNELYAGEKSKIALRAYKKELHLELKNILSEYEM 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                               40 KLTSSIEYKRH-----GDDYAKYAERIAEELQYY---GSNSFASFIKGEGVLYKEIL
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                                                                                                                                                                                                                53;
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                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:::|::|::|GLDVLEIEPPMMKNHPLLSIKNKENLIITPHVAWASKEALNA 294
                                                                                                                                                                                                      37;
                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                             Query Match 7.6%; Score 97.5; D
Best Local Similarity 23.0%; Pred. No. 6;
Matches 37; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%; Score 97.5; D
25.4%; Pred. No. 18;
tive 27; Mismatches
C,Superfamily: phosphoglycerate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SLEEMDDREVKEMCDELSIKNTDNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, 2004, 03:13:15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 LSKILERSLEEMDDEE---
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Best Local Similarity 25.4%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-728 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary A; Molecule type: DNA
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GenCore version 5.1.6
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OM protein - protein search, using sw model

5, 2004, 03:08:23 ; Search time 12 Seconds (without alignments) 1097.812 Million cell updates/sec July Run on:

US-09-732-091-4 1279 1 MAYKYDRDLEFLKQLESSDL......LRLKTQQANGDKKSLQIESI 253 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	026107 helicobacte								aquifex ae		_				P31956 arthrobacte	P46064 caenorhabdi	P77994 thermotoga		O99kx7 equus cabal						P45274 haemophilus			033662 streptococc		~		_	705 sus
SUMMARIES	ID	YF88 HELPY	YF88 HELPJ	YF87 HELPY	YF87 HELPJ	YAAW ECOLI	YAAW ECO57	HS9A BRARE	SECA_TREPA	BIOF AQUAE	ABIC LACLA	YC09_CAMJE	BPA1 HUMAN	REST_CHICK	PAC BACME	PAC ARTVI		RPSD THEMA	GATB_METJA	HS9A HORSE	YJK9 YEAST	TPM1_CIOIN	LA BOVIN	Y705_CHLPN	GATE_SULSO	AMPN HAEIN	NESG_HUMAN	HS9A_CRIGR	RPSD STRMU	SSM4 SCHPO	HS9A CHICK	HS9A HUMAN	HS9A MOUSE	HS9A_PIG
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1 MAYKYDRDLEFLKÇLESSDLLDLFEVLVFGKDGEKRHNEKLISSIEYKRHGDDYAKYAER 60 1 MAYKYORDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER

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## ALIGNMENTS

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PRT;	Created) Last sequence update) Last annotation update) [P1588.	ylobacter py Epsilonprot bacter,	2, 9252185; K.A., Klenk Cahou L., Klenb Dodson R., M. Lee N., Teterback T., Fujii C., Karp P.D.,	ince of the	s copyright. It is itute of Bioinform itus Institute. T stitutions as long ment is not remove ense agreement (Se ense@isb-sib.ch).	; 74. lete proteome. Mw; 00El5A38B1A2036A	<pre>%; Score 1279; DB 1; %; Pred. No. 9.1e-88; 0; Mismatches 0;</pre>
STANDARD;	(Rel. 40, (Rel. 40, (Rel. 40, protein E	Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; Epsilonproteobacteria; Helicobacteraceae; Helicobacter. NCBI TAXID=210;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=97394467; PubMed=9252185; MEDLINE=97394467; PubMed=9252185; MINTED JF., White O., Kerlavage A.R., Clayton R.A., Fleischmann R.D., Ketchum K.A., Klenk HP., Gill & Nelson R., Quackenbush J., Zhou L., Kirkness E.F., McTenney K., PitzGerald L.M., Lee N., Adams M.D., Berg D.E., Gocayne J.D., Utterback T.R., Peterson. Getton M.D., Weidman J.M., Fujii C., Bowman C., Wat Clayes W.S., Borodovsky M., Karp P.D., Smith H.O., Futerer J.C.;	"The complete genome sequence of the gastric p pylori."; Nature 388:539-547(1997). -1- SMILARITY: Belongs to the UPF0174 family.	OT entry is c Swiss Institu Bioinformatic profit insti this statemen ires a licens	656; AAD08627.1; - ; D64718. 18, - 18, - 18, - 18, - 1970134; UPP0174. 67; UPP0174; L 1 protein; Complet. 253 AA; 28417 MM;	100.0%; larity 100.0%; Conservative
RESULT 1 YF88_HELPY ID YF88_HELPY AC 026107;	2001 2001 2001 2001 tical	Helicobacter py Bacteria, Prote Helicobacterace NCBI_TaxID=210;	STEALUNCE FROM N.A. STEALUNCE STEALU	"The complete genome seq pylori."; Nature 388:539-547(1997)	This SWISS-PR between the the European use by non- modified and entities requ	EMBL, AE000656; AAD08627.1; PIR; D64718; D64718. TIGR; HP1588; InterPro; IPR005567; UPP0174. Pfam; PF03667; UPP0174; 1. Hypothetical protein; Complete SEQUENCE 253 AA; 28417 MW;	/ Match Local Simi ee 253;
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1. protein; Complete proteome.
209 AA: 23069 MW; F98D3FB8F3F62323 CRC64;
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Matches 123; Conservative 33; Mismatches
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Nature 388:539-547(1997).
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Unpublished observations
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Hypothetical protein; Co
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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16-0CT-2001 (Rel. 40, Last sequence update)
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Hypothetical protein JHP1494.
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INT, CARBOG, ENTRO.
InterPro; IRR005367; UPF0174.
Pfam; PF03667; UPF0174; 1.
Hypotherical protein; Complete proteome.
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Mature 397:176-180(1999).
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                                                                                                                                                                                                                                                     241 ANGDKKSLQIESI 253
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62 NYNESSATSLIEQNWLSKLIKDSLEKWSRREIKELCNELGMTNIDKVIGENKQVLIASTL 121
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STRAIN=26695 / ATCC 700392;
STRAIN=26695 / ATCC 700392;
Comb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,
Loftus B., Richardson D., Dodson K., Khalak H.G., Glodek A.,
McKenney K., FizzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.B., Googayne J.D., Utterhack T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Mallin B.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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NCBI_TaxID=562;
                                                                           YAAW OR BOO11
                                                                                                                                                                                                                      SEQUENCE
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TLFKMGGFKSYQLAVIVANAVAKTILGR-GLSLAGNQVLTRTLSFLTGFVGWIITGVWTA 213
                NYNKKTETTLIEGNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLFKMGGFKSYQLAVIVANAVAKTILGRGL-SLAGNQVLTRTLSFLTGPVGWIITGVWTA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 NEKLTSSIBYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NEELTSLTEYQRYGHDYAKYPRRIAEELQRYGGNSFANFFRDEGVLYKEILCDACDHLDI
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.
Smith D.R., Nochan B., Guild B.C., deJonge B.L., Garmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                             two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 protein; Complete proteome.
209 AA; 22907 MW; C6EC950CDD424CAF CRC64;
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59.8%; Pred. No. 7.7e-40;
iive 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                          "Genomic sequence comparison of two unrelated igastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                                                                                                  Last sequence update)
                                                                                                                                  209 AA.
                                                            IDIAGPAYRVTIPACIVVATLRLK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 IDIAGPAYRVTIPACIVVATLRLK 237
                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last sequ
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001571; AAD07072.1; -. PIR; A71800; A71800.
                                                                                                                                                                                          Hypothetical protein JHP1493.
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Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Complete
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Best Local Similarity
                                                                                                                                                                                                                                                    NCBI_TaxID=85963;
                                                                                                                                                                  16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 VIVANAVAKTILGRGLSLAGNOVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 YLNDSDLDFLQHCSEEQLANFARLLTHNEKGKTRLSSVLMRNELFKSMEGHPEQHRRNWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FARM.
SEQUENCE FARM.
SEQUENCE FIRE.
MEDLINE=87426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE=94003405; PubMed=8400364;
James R., Dean D.O., Debbage J.;
"Five open reading frames upstream of the dnaK gene of E.
DNA Seq. 3:327-332(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein, Complete proteome. CONFLICT 190 L -> F (IN REF. 1). SEQUENCE 237 AA, 26665 MW, A36682B2EAl16747 CRC64,
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125 TWKKMDEEHKQEFLHAVDARVNELEELLPLLMKDKLLAKGVS---
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                    P75617; Q47290;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
Hypothetical protein yaaW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X67700, CAA47934.1; -.
EMBL, AECO112; AAC73122.1; -.
PIR, C64721, C64721.
CGGene, EG14340; yaaw.
InterPro, IPR063567; UPF0174.
Pfam; PF03667; UPF0174; 1.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                            Escherichia coli.
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LOIACLR :
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RESULT

RESULT 5 YAAW\_ECOLI

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61; Conservative
                                                                                                                   STANDARD;
                  235
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                                                                                                                                                                                                                                                                Danio.
                                   223 LOIACLR
                229 IVVATLR
                                                                                                                                                                                                                                                                Cyprinidae; Dani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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                                                                                                                   BRARE
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090474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --EVKEMCDELSIKNTDNINRQALSAATLTLFKWGGFKSYQLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 VIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKYDRULEFIKQLESSDILDIFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han. C.G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Taraka M., Tobe T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLNDSDLDFLQHCSEQLANFARLLTHNEKGKTRLSSVLMRNELFKSYRGHFEQHRRNWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Gaps
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDREA N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett T., Klink S., Boutin A., Shao X., Miller L.,
Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Weich R.A., Blatther F.R.;
Weiche Sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Efam; PF03667; UPP0174; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 237 AA; 26681 MW; A25482B2EA116759 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the UPF0174 family.
                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Hypothetical protein yaaw.
Fysh OR 20011 OR ECS0012.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                          Enterobacteriaceae; Escherichia
NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005178; AAG54311.1; -. EMBL; AP002550; BAB33434.1; -.
             STANDARD;
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PIR; C90630; C90630.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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            YAAW ECO57
P58316;
YAAW ECOS7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 DYVSRMKDTQKHIYYITGETKDQVANSAFVERLRKAGLBVIYMIEPIDEYCVQQLKEYDG 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 KTETTLIEGNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRGALSAATLTLFKMGG 161
                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopierygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the zebrafish and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 LDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the heat shock protein 90 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%; Score 105; DB 1; Length 726; 21.4%; Pred. No. 2.5; ive 41; Mismatches 75; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 36-136 FROM N.A.
MEDLINE=95071389; PubMed=7980538;
Krone P.H., Sass J.B.;
"HSP 90 alpha and HSP 90 beta genes are present in the zebz are differentially regulated in developing embryos.";
Biochem. Biophys. Res. Commun. 204:746-752(1994).
-i. FUNCTION: Wolecular chaperone. Has ATPase activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL, 135586; AAA9518.1; ...
PTR; JG2343; JC2343.
HSSP; PO7900; LBYO.
LETN; ZDB-GENE-990415-94; hsp90a.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
InterPro; IPR01404; Hsp90.
InterPro; IPR0183; HSP90; I.
PFam; PP0183; HSP90; I.
PRINTS; PR00775; HEATSHOCK90.
SWART; SM00387; HATPase c: 1.
PROSITE; PS00299; HSP90; I.
Chaperone; ATP-binding; Heat shock.
SEQUENCE 726 AA; B3361 MM; F7DEB8EFIFBC9CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lele Z., Hadfi S., Sass J.B., Krone P.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                          75-JTJ-1999 (Rel. 38, Created)
15-JTJ-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HSP90A, OR HSP90.
726 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF068773; AAC21567.1; -.
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us-09-732-091-4.rsp

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                                                                                                                     -----IMKDILDKKIEKVTVSNRLVSSPCCIVTSTYGWTANMERIMKSQALR 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Involved in protein export. Interacts with the secY/secE subunits. SecA has a central role in coupling the hydrolysis of ATP to the transfer of pre-secretory periplasmic and outer membrane proteins across the membrane (By similarity). SUBUNIT: Part of the prokaryotic procein translocation apparatus which comprise secA, secB, secB, secE, secG and secY (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.,
                                                       162 FKSYQLAVIVANAVAKTILGRGLS--LAGNQVLTRTLSFLTGPVGWIIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sımılarıry).
SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                      ----GVWTA---IDIAGPAYRVTIPACIVVATLRLKTQQANGDK 245
----NLVS-VTKEGLELPEDEREKKKQDELKAK-YENLCK-
                                                                                                                                                                                                                                                       615 DNSTMGYMTAKKHLEIN-----PAHPIVETLREKAEAEKNOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916 AA; 103779 MW; EA5561F6EE7C65AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Preprotein translocase secA subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \operatorname{similarity}. SIMILARITY: Belongs to the secA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP
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InterPro; IPR000185; SecA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02810; SEC-C; 1.
Pfam; PF01043; SecA_protein; 1.
PRINTS; PR00906; SECA.
TIGREAMs; TIGR00963; secA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE001217; AAC65365.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Spirod
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECA OR TP0379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
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                                                                                                                           568
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Length 916;

Score 97; DB 1; Pred. No. 13;

7.6%;

Best Local Similarity

Query Match

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13;
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                                                                                                                104
                                                                                                                                                                                            147
                                                                          367
                                                                                                                                                                                                            1. | : : | : : : | : : : | : : | 1. 416 WVVLPTNLPVARVDEHDVVYLSEEEKWSAICDEIKEAHTRGQPVLVGTISIEKSEKLS-- 473
                                         48
                                                                                                                                                                                                                                                                   189
                                                                                                                                   EH-----IRIAQRNRTWATITFQNFFR-----WYKCLSGWTGTADTEALELNKIYKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-amino-7-cxononanoate + CoA + CO(2).
-!- COPACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Biotin biosynthesis; first step.
-!- PATHWAY: Biotin biosynthesis; first step.
-!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent aminotransferases.
                                         ---KRHNEKLTSSIEYK
                                                                          311 FKY---IHYFTQALRAHLLYRADVDYVVKDGQVQIVDEFTGRILEGRRYSDGLHQAIEAK
                                                                                                              RHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEI--LCDVCDKLKVNYNK--KTE
                                                                                                                                                                                          -LSIKNTENLNRO
                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY_2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxononancate synthase (EC 2.3.1.47) (AONS) (8-amino-7-ketopelargonate synthase (C 2.3.1.47) (AONS) (8-amino-7-AONT)
7-KAP synthetase) (7-keto-8-amino-pelargonic acid synthetase)
7-KAP synthetase) (L-alanine--pimelyl CoA ligase).
Aquifex aeOlicus.
       Gaps
                                                                                                                                                                                                                                                                   ---VAKTILGRG--LSLAGN
                                                                                                                                                                                                                                                                                                    -----ALLRIRGVKHEVLNAKNHAREALIIAEAGAKGSVTIATNMAGRGTDIKLGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98196666; PubMed=9537320; Deckert G., Warren P.V. Gasaterland T., Young W.G., Lenox A.L., Grekert G., Warren P.V., Gasaterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRIDOXAL PHOSPHATE (BY SIMILARITY).
     16;
   Indels
                                                                                                                                                                                      105 TILIEQNM-LSKILERSLEEMDDEEV-KEMCDE--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004723; BioF.
Pfam; PF02490; ALA synthase; 1.
Pfam; PF0155; anthotran 1.2; 1.
TIGRRAMS; TIGR00859; hioF; b.
PROSITE; PS00599; AA TRANSFER CLASS 2; 1.
Biotin biosynthesis; Transferase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42532 MW; 536B34A5D5F84401 CRC64;
   67;
                                                                                                                                                                                                                                                               148 ALSAATLTLFKMGGFKSYQL-----AVIVANA
                                                                                                                                                                                                                                                                                                                                                                                                   Ą
   Mismatches
                                     3 YKYDRDEEFLKQLESSDLLDLFEVLVFGKDGE-
                                                                                                                                                                                                                                                                                                                                                                                                 373
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HSSP: P12998, 1BSO.
InterPro; IPR003408; Ala synthase.
InterPro; IPR004839; Aminotrans_1/II.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001917; Aminotrans II.
   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000699; AAC06836.1; -.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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BINDING 223
52;
                                                                                                                                                                                                                                                                                                                                                                                               BIOF AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VF5;
                                                                                                            49
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F_AQUAE
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     --- OKVELVISRO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AYKYDRDIEFIKQIESSDILDIFEVIVPGKDGEKRHNEKLTS-SIEYKRHGDDYAKYAER 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 TETTLIEQNMISKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGF
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN.NCTC 11166;
MEDINEZCTC 11166;
MEDINEZCTC 11166;
MEDINEZCO150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668 (2000).
                                                                                                                                                                                                                                                                                                                     Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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                                                    7.4%; Score 95; DB 1; Length 517;
145 FINDYNIDIGNGLDFRFNLFESNQWFSITYNSSKYKGKN-LIKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the UPF0144 family.
-!- SIMILARITY: Contains 1 HD domain.
-!- SIMILARITY: Contains 1 KH domain.
                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0144 protein Cj1209.
                                                                                            163 KSYQLAVIVANAV-AKTILGRGLSLAGNOV 191
                                                                                                                                                                                                            517 A.A.
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                                                                                                                 246 -SEELVVILINSLYVKRGLGLGIELIGTNL
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InterPro; IPRC036675; Unchar_HDIG.
Pfam; PF01066; HD; 1.
Pfam; PF000013; KH; 1.
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Hypothetical protein; Transme:
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HAMAP; MF_00335; -; 1.
InterPro; IPR006674; HD.
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SMART; SM00322; XH; 1.
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517 AA;
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                                                                                                                                                                                                          CAMJE
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Q9PNB6;
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YC09 CAMJE
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                                                                                                                                                                                                                        119 ASIIDGVRLSKAQKRVFKHKDYBELBEFLK----KNRKKFRRVLI--ITDTVFSMDGDVA 172
                                                                                                                                                                                                                                                                                               173 DLKRLTQICEEYDCMLYIDEAHTTGTIGKGGLDYFGIEHKEYIIVMGTLSKALGSYGAFV 232
                                                                                                                                   BRIABEL-QYYGSNSFASFIKG-------EGVLYKEILCDVCDKLKVNYNKKTE 104
                                                                                                                                                                                                                                                                  --FKSYQLAVIVANAVAKTILGR-GLSLAGNQ-----VLTRTLSFLTGPWGWII 207
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                                                                                         TILIEQNALSKILERSLEEMDDEEVKEMCDELSIKNIDNLNRQALSAATLILFRAGG---
                                          Gaps
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                                                                                                                                                                   RELERKLASFKGTESCVLFGSGFLANVGTIPALVEEGDL---VLSD----ELNH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durmaz E., Higgins D.L., Klaenhammer T.R.;
"Molecular characterization of a second abortive phage resistance
gene present in Lactococcus lactis subsp. lactis ME2.";
                                        77;
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             Length 373;
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      Score 96.5; DB 1; Length 37
Pred. No. 4.7;
); Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
                                                                                                                                                                                                                                                                                                                                                             233 CGTKLLID-----YLVNKARSLIPST-SLPPSVCAGAKKAIEI 269
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                                                                       9 LEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHG-
                                                                                                                                                                                                                                                                                                                                 TGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGDKKSLQI
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                                        64; Conservative
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ID ABIC_LACLA
      Query Match
Best Local S:
Matches 64
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Stanley J.R.;
 161
           -- DWCDKLKVNYNKKTBTTL-- 107
                              ---KÉYLCKSOKHIONLOSDV-DKLKNKYOBKLDDVLKI 140
                                                                   201 BFAAERLINVINKADELKGRIIGKEGRNV--KTLE-----MVLGVDIIID-----
                                                     --IEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGG
                                                                                               FKSYQLAVIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=93346896; PubMed=8345227;
Elgart G.W., Stanley J.R.;
"Cloning of the 5' mRNA for the 230-kD bullous pemphigoid antigen by
                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Bullous pemphigoid antigen 1 isoforms 1/2/3/4/5/8 (230 kDa bullous pemphigoid antigen) (Hemidesmosomal plaque protein) (Dystonia
                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Keratinocytes;
MEDLINE=92011493; PubMed=1717441;
Sawanura D., Li K., Chu M.-L., Uitto J.;
Sawanura pemphigod antigen (BPAG1). Amino acid sequences "Human bullous pemphigod antigen (BPAG1). Amino acid sequences deduced from cloned coNRs predict biologically important peptide segments and protein domains.";
                                                                                                                                                                                                                     BPA1 HUMAN STANDARD; PRT; 3214 AA.
Q03001; Q12825; Q13266; Q13267; Q13775; Q96J76; Q96QT5; Q9UGD7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Keratinocytes;
MEDLINE=91286285; PubMed=1712022;
Tanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-645 FROM N.A. (ISOFORMS 1 AND 2).
TISSUB-Fetal brain, and Retina;
MEDLINE=96121394; PubMed=8575775;
Brown A., Dalpe G., Mathieu M., Kothary R.;
"Cloning and characterization of the neural isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Pineal gland;
Geerts D., Sonnenberg A.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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           IAEELQYYGSNSFASFIKGEGVLYKEILC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rapid amplification of cDNA ends.";
J. Invest. Dermatol. 101:244-246(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1082-3214 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM 3).
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                                                                                                                                                                                                                                                                                                        musculorum protein) (Fragment)
BPAG1 OR DMH OR DT OR KIAA0728
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                                                                                                                                         222 RVTIPACIVVATLRL 236
                                                                                                                                                        --DIPGAIIVSCENL 257
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                                                                                                                                                                                                                   STANDARD;
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                                LOOBBEKLKED
                                                                                                                                                                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
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"Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion junction plaque proteins.".

J. Biol. Chem. 26:12555-12559 (1991).
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                                                                                                                              SEQUENCE OF 2160-2767 FROM N.A.
MEDLINE=91216368; PubMed=2090522;
Owaribe K., Kartenbeck J., Stumpp S., Magin T.M., Krieg T.,
Diaz L.A., Franke W.W.;
"The hemidesmosomal plaque. I. Characterization of a major
constituent protein as a differentiation marker for certain forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSP_005056, VSP_005057, VSP_0050597,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2462-3214 FROM N.A. (ISOFORM 8).
MEDLINE=94280413; PubMed=8010969;
Hopkinson S.B., Jones J.C.;
Hidentification of a second protein product of the gene encoding human epidermal autoantigen.";
Biochem. J. 300:851-857(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of cytoplasmic bullous pemphigoid antigen (BPAG1). Empirical localization of the N-terminal globular domain-rod boundary.";
J. Biol. Chem. 271:9716-9722(1996).
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IsoId=Q03001-4; Sequence=VSP_005054, VSP_005056;
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-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=10;
Comment=Isoforms 1, 2, 5 and 8 are or may be
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 2287-3214 FROM N.A. (ISOFORM 5)
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IsoId=Q03001-3; Sequence=VSP_005058,
VSP_005051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q03001-1; Sequence=Displayed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=6; Synonyms=EA; IsoId=094833-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8WXK8-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB=Keratinocytes;
MEDLINE=89067122; PubMed=2461961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96199235; PubMed=8621649;
                                                                                                                                                                                                                                                                                                                              Differentiation 45:207-220(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=7; Synonyms=EB;
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                                                                                                                                                                                                                                                                                                  epithelia.
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7.48;
                                46; Conservative
                                                                                                                                                                            STANDARD;
       1143
                                                                                                                                                                                                                            Gallus gallus (Chicken)
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
       1091
                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                           2252 E 2252
                                                                                                                              147 0 147
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      DOMAIN
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REST_CHICK
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                         FXOSILE; FSUULLY; ACTIMIN 1; I.
PROSITE; PSUOD20; ACTIMIN 2; FALSE NEG.
PROSITE; PSSO021; CH; Z.
Antigen; Actin-binding; Coiled coil; Repeat; SH3 domain;
Structural protein; Cytoskeleton; Cell adhesion; Calcium;
Calcium-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENTRAL FIBROUS ROD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLOBULAR 2.
ACTIN-BINDING
                    IsoId=094833-1; Sequence=External;
        lsoId=094833-3; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                             GLOBULAR 1
                                                                                                                                                                                          AL096710, -; NOT ANNOTATED CDS.
AY032900; AAK63130.1; -.
                                                                                                                                                                EXBL: M69225; -; NOT ANNOTATED_CDS.
EMBL: 111690; AAACS288.1; -.
EMBL: U31850; AAACS228.1; -.
EMBL: U31851; AACS0243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
3
3
3
                                                                                                                                                                                                         AY032901; AAK63131.1; -.
                                                                                                                                                                                                              EMBL, M63618; AAA35606.1;
EMBL; X58677; CAA41528.1;
EMBL; M22342; AAA35538.1;
EMBL; U04850; AAA57184.1;
                                                                                                                                                                                                                                        EMBL, U04850, AAA57185.1;
PIR, 156317, A40937.
Genew; HGNC:1090; BPAG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1669
                                                                                                                                                                                                                                                              MIM; 113810; -.
MIM; 600088; -.
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215
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              Name=10
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DOMAIN
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EMBL; A
EMBL; A
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2075 SPRDEKELERLOICORKSDHLKEOFEKSHEQLLONIKAEKENNDKIORLNEELEKSNECA 2134
                                                                                                                                                                                                                            98 -NYNKKTETTLIEQNMLSKI--LERSLEEMDD--EBVKEMCDELSI-----KNTDNLNR 146
                                                                                           2 AYKYDRDLBFLK--OLESSDLLDLF----BVLVFGKDGEKRHNEKLTSSIEYKRHGDDYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-98137792; PubMed-9469933; Gripharic L., Volosky J.M., Keller T.C. III; "Cloning and expression of chicken CLIP-170 and restin isoforms."; Gene 206:195-208(1998).
                                                       38;
Score 95; DB 1; Length 3214;
                                                                                                                                                                                          56 KYAERIAEEL--QYYGSNSFASFIKGEG---VLYKEILCDVCDKLKV--
                                                       62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=042184-2; Sequence=VSP 000761;

Name=3; Synonyms=CLIP-170(11);

Isold=042184-3; Sequence=VSP 000762, VSP_000763;

Name=4; Synonyms=CLIP-170(11+35);

Isold=042184-4; Sequence=VSP 000764;

-!- SIMILARITY: Contains 2 CAP-Gly domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            042164, 042228, 057563, 057564, 15-70L-1998 [Rel. 36, Created) 15-70L-1998 [Rel. 36, Last sequence update) 16-00T-2003 [Rel. 42, Last amotation update) Restin (Cytoplasmic linker protein-170) (CLIP-170).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 17-1139 FROM N.A. (ISOFORMS 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event-Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment=Additional isoforms seem to exist;
               IsoId=C42184-1; Sequence=Displayed;
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This SWISS-PRCT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN-- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12114980;
Yang S., Huang Y.H., Huang X.D., Li S.Y., Yuan Z.Y.;
"High expression of penicillin G acylase gene from Bacillus megaterium
in Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KYDROLEFLKQLESSDLLDLFEV--LVFGKDG-----EKRHNEKLTSSIEYKRHGDDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 237542; CAABST74.1; -
EMBL; AF161313; AAD45609.1; -
PIR; 49925. S49252.
MEROPS; 5455.001,
InterPro; IPR002692; Peptidase S45.
Ffam; PF01804; Penicil amidase; 1.
Ffydrolase; Antibiotic resistance; Zymogen; Calcium-binding; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                   anion +
                                                        STRAIN=ATCC 14945, PubMed=7875576; Martin L.M., Prieto A.M., Cortes E., Garcia J.L., Martin L.M., Prieto A.M., Cortes E., Garcia J.L., "Cloning and sequencing of the pac gene encoding the penicillin acylase of Bacillus megaterium ATCC 14945."; FEMS Microbiol. Lett. 125:287-292(1995).
                                                                                                                                                                                                                                                                      Acta Biochim. Biophys. Sin. 31:601-603(1999).
-!- CATALYTIC ACTIVITY: Penicillin + H(2)O = a fatty acid anion aminopenicillanate.
-!- COFACTOR: Binds 1 calcium ion per subunit (Potential).
-!- SUBURIT: Heterodimer of an alpha chain and a beta chain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENICILLIN G ACYLASE BETA SUBUNIT.
BY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 93.5; DB 1; Length 802; 1.8%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (A -> YKS (IN STRAIN CA4098)
877CA0564E50DFBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 21.8%; Pred. No. 20;
Conservative 39; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALLION (TOTENTIAL).

T -> M (IN STRAIN CA4098).

T -> E (IN STRAIN CA4098).

T -> S (IN STRAIN CA4098).

T -> S (IN STRAIN CA4098).

S -> N (IN STRAIN CA4098).

C -> P (IN STRAIN CA4098).

O -> P (IN STRAIN CA4098).

I -> A (IN STRAIN CA4098).

I -> A (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).

T -> K (IN STRAIN CA4098).

NAA -> YKS (IN STRAIN CA4098).
                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLUTAR LOCATION: Extracellular (Potential).
-!- SIMILARITY: Belongs to peptidase family 845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENICILLIN G ACYLASE
PENICILLIN G ACYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPACER PEPTIDE
            Misainmurhag Hoiji 32:215-221(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U07682; AAB41343.1; -.
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524
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265
802
266
177
341
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Best Local Similarity
'Thes 62; Conserva
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     789
802 AA;
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                                                                            STRAIN=CA4098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT SITE
METAL
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VARIANT
SEQUENCE
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            엄
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      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1072 ABEVLQ-----TMEKVTKEKDAIHQEKIETLASLENSRQINBKLONELDMLKQNNLKNBE 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1127 ELTKSKELLNLENKKVEELKKEF-----EALKLAAAQ------KSQQLAALQEE 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IABELQYYGSNSFASFIKGEGVLYK---BILCDVCDKLKVNYNKKTETTLIEQNMLSKIL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E----RSLEEMDDEEVKEMCDELSIKNTDNLARQALSAATLTLFKMGGFKSYQLAVI-VA 172
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                                                                                                                                                                                                                   Coiled coil; Repeat; Alternative splicing. CAP-GLY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAC BACME STANDARD; PKI; GUC AA...
060136; Q9S463;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Penicillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                              TOTKLEHARIKELEGSLLFEKTKADKLORELEDTR
                                                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSF (in isoform 3).
/FTIG=VSP 000763.
T -> RRRQISEDPENT (in isoform 4).
FTIG=VSP 000764.
F -> R (IN REF. 2; AAC03547).
E -> V (IN REF. 2; AAC03549).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94.5; DB 1; Length 1433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECURNCE FROM N.A. STRAIN-ATCC 14945; KANG J.H., Kim S.J., Park Y.C., Hwang Y., Yoo O.J., Kim Y.C.; "Nucleotide sequence of the penicillin G acylase gene from Bacillus megaterium and characteristics of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; 5631CE8683498E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus megaterium.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                  RQISEDPEN (in isoform 3)
/FTId=VSP_000762.
                                                                                                                                                                                                                                                                                SER-RICH.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.4%; Pred. No. 34; ive 36; Mismatches
entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                   FTIG=VSP
                                                                                                                                                                                                                                                   SER-RICH.
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                                          EMBL, AF014012; AAC60344.1; EMBL, AF020764; AAC60345.1; EMBL, AF045651; AAC60345.1; EMBL, AF045651; AAC03548.1; InterPro; IPR000938; CAP-GJY, InterPro; IPR001938; CAP-GJY, InterPro; IPR001938; CAP-GJY, INTERPRO; IPR001938; CAP-GJY, FO03178; SMART; SM0343; ZAF_CC370; IPROSITE; PS00845; CAP_GIY_1; 2. PROSITE; PS00845; CAP_GIY_1; 2.
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                                                                                                                                                                                                                 Cytoskeleton; Microtubule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 24.4
52, Conservative
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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RESULT 14
PAC BACKE
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89 SKDEQSRRDGYSNKEIKKWIDGLDRQPKELIAKFAEGISRYVWEALKOPDDKLSKEFHEY 148
                                                   -KILERSLEEMDDEEVKEMCDELSIKN- 140
                                                                                                                    -----TDNINRQALSAATLTLFKMGGFK-----SYQLAVIVANAVAK 177
                                                                                                                                             209 PSAPTSIVSEGKPKRDSSSQSLQILSSAVIKASEKVGKERENFVQTSEELGLPIKIGSNA 268
                                                                                149 QFLPQKWTSTDVVRVYMVSMTYFMDNHQELXNAEILAKLEHEYGTEVSRXXFDDLVWKND
                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pentcillin G acylase precursor (EC 3.5.1.11) (Penicillin G amidase)
(Penicillin G amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; 545.001;
InterPro; IPR002692; Peptidase_S45.
Pfam; PF01804; Penicil amidase; 1.
Hydrolase; Antibiotic resistance; 2ymogen; Calcium-binding; Signal.
Hydrolase; Antibiotic resistance; 2ymogen; Calcium-binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94259306; PubMed=8200542; Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V., Konstantinovic M., Marjanovic N., Ljubijankic G., Glisin V., The penicillin amidase of Arthrobacter viscosus (ATCC 15294)."; Gene 143:79-83(1994)."; -i- CATALYTIC ACTIVITY: Penicillin + H(2)O = a fatty acid anion aminopenicillanate.
-i- COPACTOR: Binds I calcium ion per subunit (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENICTILIN G ACYLASE ZYMOGEN.
PENICTLLIN G ACYLASE ALPHA SUBUNIT.
SPACER PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENICTILIN G ACYLASE BETA SUBUNIT.
BY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Arthrobacter viscosus.
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=1673;
                                                                                                                                                                                    178 TILGRGLSLAGNQVLTRTLSFLTGP-VGWIITGVWTAIDIAGPAY 221
                                                                                                                                                                                                           269 AIVGSEKSATGNALL----FSGPQVGFVAPGFLYEVGLHAPGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to peptidase family S45.
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PIR; I39665; I39665.
HSSP; P06875; LAJQ.
                                                                                                                                                                                                                                                                                                           STANDARD;
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265
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802 AA;
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Gaps

17;

7.2%; Score 92.5; DB 1; Length 802; llarity 21.8%; Pred. No. 24; Conservative 39; Mismatches 107; Indels 77

62;

Best Loca

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89 SYDEQSRRDGYSNYRIXKWIDGLDRQPRELIAKFAEGISRYVNEALKDPDDKLSKEFHEY 148
                                                                                                                     ----KKTETTLIEQNMLS------140
                                                                                                                                      KYAERIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN-- 100
                                                                                                                                                                               ------TDNLNRQALSAATLTLFKMGGFK-----SYQLAVIVANAVAK 277
                                                                                                                                                                                                 209 PSAPTSIVSEGKPKRESSSQSLQKLSSAVIKASEKVGKERENFVQSSEELGLPLKIGSNA 268
                     55
4 KYDRDLEFLKOLESSDILDLFEV--LVFGKDG-----EKRHNEKLTSSIEYKRHGDDYA
                                                                                                                                                                                                                                     178 TILGRGLSLAGNQVLTRTLSFLTGP-VGWIITGVWTAIDIAGPAY 221
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098qt2 mycoplasma 08.127 plasmodium 08.1144 plasmodium 09pic9 campylobact 09pi94 campylobact 09arg9 oryza sativ 09arg9 oryza sativ

Q99ud0 staphylococ

Q81eq5 plasmodium O61768 cenorhabdi Q97mm5 clostridium Q81122 plasmodium Q8tpc2 methanosarc Q8tpc2 methanosarc Q8tb57 fusobacteri Q94188 borrelia bu Q94189 malus domes Q81589 plasmodium Q97uf7 sulfolobus Q97uf7 sulfolobus Q51577 borrelia bu

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Q9ppg7 Q8e6j7 Q8e143 Q96xt6 Q886n2

07y5e5 aeromonas p 061767 caenorhabdi

us-09-732-091-4.rspt

July .

Run on:

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Q980TC
Q81297
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Q91294
Q92ARQ9
Q82RQ5
Q81EQ5
Q81EQ2
Q81EQ2
Q81EQ2
Q84ES3
Q94ES3
Q94ES3
Q94ES3
Q95ES8
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                                                                                               Q8S6N2
Q9PPG7
Q8E6J7
Q8E143
Q96XT6
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                                                                               1017041
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1279
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Scoring table:

Searched:

Database

Perfect score:

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### ALIGNMENTS

RESULT 1  QBXGV3  ID QBXGV3  AC QBXGV3  AC QBXGV3  DT 01-MAR-2002 (TrEMBLrel. 20, Created)  DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  DT 01-MAR-2003 (TrEMBLrel. 24, Last amnotation update)  DT 01-MAR-2003 (TrEMBLrel. 24, Last amnotation update)  DF 01-UNN-2003 (TrEMBLrel. 24, Last amnotation update)  DF 10-UNN-2003 (TrEMBLrel. 24, Last amnotation update)  CN 10-UNN-2003 (TrEMBLrel. 20, Last sequence of Sigma 32)  CN 2010 OR HTGA ON STROOTO  CN 2010 OR HTGA ON ST		
5: sp_intwart:*  6: sp_intwart:*  7: sp_mammal:*  8: sp_mbage:*  9: sp_bage:*  10: sp_land:*  11: sp_voints:*  13: sp_virus:*  14: sp_unclassified:*  15: sp_rvirus:*  16: sp_acteriap:*  17: sp_archeap:*	Fred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  Ouery  No. Score Match Length DB ID  Description	1         265         20.7         237         16         208XGV3         208XGV3         28Ammonella           2         266         20.3         237         16         2083SS4         Q88AT4         shigella fl           4         133         10.4         39         16         20E1C7         Q861C7         escherichia           5         10.5         8.2         1245         5         20E1AN1         Q81A1         Q81A1         Q81A1         Q81A2         thermoanaer           6         10.2.5         8.0         1590         5         Q8MX30         Q841A4         Spnechoocc         Q8 A24         thermoanaer           9         10.2.5         8.0         1590         5         Q8MX30         Q8 A2A         thermoanaer         Q8 A2A         thermoanaer           10         10.2.5         8.0         1590         5         Q8 MX30         Q8 MX30

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MEDLINE=22590274; PubMed=12704152;
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ses 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6C RENNWOLLAGEFOHYGGDSIANKLRGHGKQYRAILLDVAKELKLKADKSMSTFEIEQQLLE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 KILERSLEEMDDEEVKEMCDELSIKATDNIARQALSAATLTIFK-MGGFKSYQLAVIVAN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 HFLRHTWQRWDAAHKQBFLQAVDAKVSELEELLPLLMKDRSLAKGVSHLLSTQLTRILRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVAT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 HAAMSILGHGL-LRG------AGLGGPVGAALNGVKA---MSGSAYRVTIPAVLOIAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKR-----HNEKLTSSIEYKRHGDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VTYLHDEDLDFLQHCSEEQLADFARLITHNEKGKARLSSVLSHNE-LFKAME--GHPEQH
                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Bakera S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mitchead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Ipphi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=3C1 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang J., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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20.7%; Score 265; DB 16; Length 237;
Best Local Similarity 32.6%; Pred. No. 2.6e-12;
Matches 79; Conservative 40; Mismatches 101; Indels 2;
                                                                                                                                                                                                                                                                                                         EMBL; AE016834; AA067744.1; -.
EMBL; AE008693; AAL18974.1; -.
EMBL; AL627265; CAD01163.1; -.
Interpro; IRF005367; UPP0174.
Efam; PF03667; UPP0174; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 237 AA; 26515 MW; 184ADE026EA5BCA9 CRC64;
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Last annotation update)
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
MEDLINE=21534947; PubMed=11677608;
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                                                                                                                                                                                                                                                                                   Nature 413:848-852(2001)
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Putative oxidoreductase.
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Shigella flexneri
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01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SLEEMDDE------EVKEMCDELSIKNTDNINRQALSAATLILFKMGGFKSYQLA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HLLSSÖLT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YXYDRDLEFLXQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=06:H1 / CPT073 / ATCC 700928,
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner P.R.,
"Extensive mossic structure revealed by the complete genome sequence
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Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Purland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner P.R., "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.", "Infect. Immun. 71.2775-2786 (2003).

EMBL; ARO15039; AAN41678.1; BMBL; ARO15039; AAN41678.1; BMBL; PRO3667; UPP0174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 TWKKWDEEHKQEFLHAVDARVNELEELLPLLMKDKLLAKGVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                        237 AA; 26709 MW; 95509A1BCB8B4CF5 CRC64;
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5727 MW; B8C190712375B31D CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL; AROHG75; AAN78516.1;
InterPro: IPR005367; UPF0174.
Fypothetical protein; Complete proteome.
SEQUENCE 237 AA; 26727 MW; B8C190712375B31D CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein yaaw.
                                                                                                                                                                                                                                                                                                                                                                                                          20.3%; Score 260; DB 16;
30.8%; Pred. No. 6.3e-12;
iive 44; Mismatches 91;
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Best Local Similarity 30.8%;
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542 EKKEEBKIMKKI-YSEHPDLVKDIMNYEKEYAEKRNILINNIKKRKTIKTIN-RYKN---- 595
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                               Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tibirso.
Thermoanaerobacter tengcongensis.
Parteria: Firmicutes; Clostridia; Thermoanaerobacteriales;
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MEDLINE=21992816; PubMed=11997336;

A Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Ya Chen Y., Xu Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., A Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

Genome Res. 12:689-700(12002)

REBL; AB013102; AAM24658.1;

GO; GO:0009424; C:ffagellar hook (sensu Bacteria); IEA.

GO; GO:0009424; E:flagellar hook (sensu Bacteria); IEA.

GO; GO:0009296; P:flagella biogenesis; IEA.

InterPro. IRR01655; Flag hook.
                                                                                                                         Seeger K., Murphy L., Harris D., Berriman M., Pain A., H
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL844507; CaD531332.1; -.
                                                                                                                                                                                                                    1245 AA; 147911 MW; D856486AFDFE4DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L protein; Complete proteome.
403 AA; 46116 MW; 60C22B9FBB51A56F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 21, Created) (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                91 VCDKLKVNYNKKTETTLIEQNMLSKILERSL----
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Thermoanaerobacteriaceae, Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 AA
                                                                                                                                                                                                                                                                                         21; Mismatches
                                                                                                                                                                                                                                                       Score 105; Di
Pred. No. 32;
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20.1%; Pred. No. 9.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 EFLKQLESSDLLDLFEVLVFGKDGEKRHNEK-
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                                                                                                                                                                                                                                                                                         35; Conservative
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hes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 DELSIKNTDNLN
 Hypothetical protein.
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                                                                                                       SEQUENCE FROM N.A.
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                                                      Eukaryota; Alveo
NCBL_TaxID=36329
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                                                                                                                                                                                                                    SEQUENCE
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                                                                                                 125 TWKKWDEEBKOEFLHAVDARVNELBELLPLIMKDKLLAKGVS-----HILSSOLF 174
                                                                                                                                                                                                                                            --EVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLA 168
                                                                                                                                                                                                                    169 VIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPAC 228
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     YKYDROLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKR---HGDDYAKYAE 59
                              RIABELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Cotton M.D., Weldman J.M., Publis C., Bowman C., Watthey D.K., Cotton M.D., Weldman J.M., Fulli C., Bowman C., Watthey L., Wallin I. Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
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Pred. No. 0.0028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein, Complete proteome.
SEQUENCE 39 AA, 4636 NM; EE53CF01F4C1C909 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HP1590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
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Nature 388:539-547(1997).
EMBL; AE000656; AAD08629.1;
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223 LQIACLR 229
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Last sequence update) Last annotation update)

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61; Conservative
             PRELIMINARY;
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                                                         01-OCT-2002
01-OCT-2002
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                                                                                                                                              ----TLTLFKMGGFKSYQLAVIVANAVAKTILGRGLSLAGNQVLTRTLSFLTGPVGWII 207
                                                                               165 HIKLAKVKDLDKPFLQDLMQKDFAEENVQKNQDKTSQLKIDKEAFIAAKBAKEEKTEKKS 224
                                                                                                                                                                                           225 FDVKQEFYFFKNEG---KPVSNLTYNSIKKS-------NDPVDRLFR-----QIV 264
                                                                                                                                                                                                                                                            ---RLKTQQ 240
                                                                                                                                                                                                                                                                                            265 DNVFVAKEKGASSVTVNLKPEİLGKLQISEKSIDGNIVATIVTESEKTKHQIBSNLSLLQ 324
---GFIKERNFTFKEIAKKISDFLKENFNIELSPEVIER 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 DRRVLAAQIQESLPELHHGHPISMEMVRLVLEGG-----AAIAISSVVRSMVVQQVARQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GRGLSTA-----GNQVLTRILSFLTGPVGWIITGVWTAIDIAGPA--- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 FAIRFAGSKLSIAPLVSRGAAMGVARLAVGRSILAFVSTALW----VWFIADLGWQAIST 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSFASFIKGEG--VLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLERMDDE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LELATEEELODLTEILF-----RRELNPLDYLTTPDPIAVQAQDRQAKLDDIBERFRFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 EVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasamoto S.,
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MEDLINE-2225144; PubMed=12240834;

MEDLINE-2225144; PubMed=12240834;

MEDLINE-22255144; PubMed=12240834;

Matanabe A. Iraneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Matanabe A., Iringohi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium Thermosynechococous elongatus BP-1.";

DNA Res. 9:123-130(2002).

EMBL, PRODS374, BAC09166.1; -.

Complete proteome
SEQUENCE 276 AA; 31282 MW; D0577A9D97E0CA92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.0%; Score 102.5; DB 16; Length 276; 19.0%; Pred. No. 7.2; ive 53; Mismatches 111; Indels 49;
                                            111 NM-LSKILERSLEEMDDEEVKEMCDELSIKNTD-----NLNRQALSAA
                                                                                                                                                                                                                                                     --VVATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus elongatus (Thermosynechococcus elongatus) Bacteria; Cyanobacteria; Chrococcales; Synechococcus. NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 NYARIIPTIFAIAQIRLLRGEQA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                               208 IGVWTAIDIAGPAYRVTIPACI---
ASDFEKVREKLEVALQ----
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                   325 AQLDLKGIKİESV 337
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Best Local Similarity 19.09
Watches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                153
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10 01-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 LYGEDGMDAHKVE-SQSIDIMMLSD--AKFQDK----YWYNSLGSSPSFTNPTESSVSM 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 MLSKILERSLEEMD-----DEEVKEMCDEL-SIKNTDNLNRQALSAATL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ETTLIEON 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 PSGGILKESFISTKVYDEILKDPATYLSKVREEYKTLMEDRHILRTEIFPNAENKIVMPV 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication From N.A.

RX Pubbed-1203239;

Rad Dacks J.B., Marinets A., Ford Doolittle W., Cavalier-Smith T.,
Logsdon J.M. Jr.;

Logsdon J.M. Jr.;

RY Pubbed-1203239;

RY Logsdon J.M. Jr.;

RY Paylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

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RY Ebylogeny, Long Branch Attraction, and the Eukaryotic Big Bang.";

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NCBI_TaxID=5762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1590 AA; 177446 MW; 5F4C7959D4D77D68 CRC64;
                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 3NA polymerase II largest subunit (Fragment).
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1590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 102; Di
22.8%; Pred. No. 73;
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                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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Gaps

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199 DDYKRHKENLEKALEKGKNNPE-------NQNAVEKAQKAEKALEKLNANNA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 ----QNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKS
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"The complete genome sequence of the carcinogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618 TMGYMTAKKHLEIN-----PTHPIVETLREKABADKNDK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                    83505 MM; 1A2A962C471CBCF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 KEYDGKNLVS-VIKEGLELPEDEDEKKKQEELNTK-FENLCK---
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
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Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
EMBL; AE011147; AAP77543.1;
Hypothetical protein; Complete proteome.
SEQUENCE 556 AA; 61984 MW; 0E48CF5376BAC48D CR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39; Mismatches
                                                                                        GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003754; F:Chaperone activity; IEA.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
Pfam; PF02518; HATPase c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 100.5; 21.6%; Pred. No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 51449 / 3B1;
MEDLINE=22709201; PubMed=12810954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                           PRINTS, PR00775; HEATSHOCK90.
SMART; SM00387; HATPARE C; 1.
PROSITE; PS00299; HSP90; 1.
SEQUENCE 726 AA, 83505 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                    EMBL; U89945; AAB49983.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Conservative
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nes 53, Conservative
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                                                            P07900; 1BYO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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SEQUENCE FROM N.A.
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01-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 LOYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYN---KKTETTLIEQNMLSKILERSL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AS014886; AAN37250.1; -. GO; GO:000353; F:sugar porter activity; IEA. GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA. InterPro; IPR002114; HPT SerP S. PROSITE; PS00589; PTS HPR SER; 1. SEQUENCE 1455 AA; 174305 MW; 36FAA1760A898F99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE-22255705; PubMed=12368864; White O., Berriman M., Hyman R.W., MEDLINE-22255705; PubMed=12368864; Milte O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Perten M.-S., Nene V., Salangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungail C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSI-EYKRHGDDYAKYAERIAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Gaps
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                                                                                                                                                                                                                                                                  Rhoptry protein, putative.
PF14_0637.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1455;
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25.5%; Pred. No. 78;
tive 29; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus tschawytscha (Chinook salmon) (King salmon)
                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                    FRT; 1455 AA
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                                                                                                                                                                 Created)
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                                                                                                                                                                                             (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                                                     01-MAR-2003 (TrEMBLrel, 23,
                                                                                PRELIMINARY;
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Nature 419:498-511(2002)
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01-OCT-2003
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1D P87397
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202
292 LIMSFL---AAWVITRL----IVGP
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                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                              MCBI TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=3D7
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AC 04363
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DT 01-JU
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DB BC-2
DB BC-2
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                ---IBQNMLSKILERSLEEMDDE---EVKEMCD----E 135
                                                                                                                             244 CNRIMCENPRITAVATOSIVASGHIAQAGFSDALIAALATLANGVIWEVKOMFEGSIDTE 303
                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 KLKVNYNKKTETTLIEQNMLSKILE--RSLEEMDDEE--VKEMCDEL-SIKNTDN---LN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 -RGYTYSLKAENRAPAEASMSAVINFVKGLQGFDSQSATIKHLVDSMVSYQNTMNQFTAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQALSAATLILFKMGG--FKSY-QLAVIVANAV-----AKTILGRGLSLAGNQVLT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YKYDROLEFLKOLESSDLIDLFEVLVFGKDGEKRHNEKLTSS----IEYKRHGDD---- 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 ------YAKYAERIAEBLQYYGSNSFASFIKGEG------VLYKBILCDWCD 93
                                                                                                  136 LSI-KNIDNLNRQALSAATIILFKMGGFKSYQLAVIVANAVAKTILGRGLSLAGNQVLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QASIDQAQAGITKVIGVLFKSADQLS---ANQVSLRIEDVDQARTLLSVWL-----VAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DC3000;
Buell R., Joadar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joadar V., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madpu R., Daughert
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.",
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 RTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQANGD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633;
                                                                                                                                                                                                                  LKSIYNGIVSYIKGEVSNLRELLGIILKSLFSAAWVSTLALE 405
                                                                                                                                                                                    195 TLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGN: PSPF02616; -.
G0; GO:0016020; C:membrane; IEA.
G0; GO:0004871; F:signal transducer activity; IEA.
G0; GO:0005935; P:chemotaxis; IEA.
G0; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004689; Chmtaxis_transd.
InterPro; IPR004689; Chmtaxis_transd.
Pfam; PF00672; HAMP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
                                                                                                                                                                                                                                                                                                                                                633 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.8%; Score 99.5; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methyl-accepting chemotaxis protein.
                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas syringae (pv. tomato)
Bacteria; Proteobacteria; Gammapro
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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             CDKLKWNYNKKTETTL-
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Best Local Similarity 23.7
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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57 -----YAERIABBLQYYGSNSFASFIKGEGVLYKBILCDVCDKLKVNYNKK----- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22255705; PubMed=12368864; Gardner M., Hyman R.W., Gardner M.J., Hall N., Fung K., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Sub B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worfedden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHN-----EKL--TSSIEYKRHGDDYAK
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:: ||:| : |:||
--LLETLKLAERVADGD 324
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
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                                                                                                                                                                                                                                                                                                                                                                                               Přío_0048.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the human malaria parasite Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 419:498-511(2002).
EMBL, ABO14829; AAN35246.1; -.
Hypothetical protein.
SEQUENCE 202 AA; 24259 WW; 48FD22A7F21165A6 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2993 (TrEMBLrel. 25, Last amnotation update)
01-CCT-2003 (TrEMBLrel. 25, Last amnotation update)
02-2 protein (Putative breast adenocarcinoma marker)
                                                                                                                                                                                                                                                             (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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7.7%; Score 99; DB E
Best Local Similarity 24.9%; Pred. No. 8.9;
Matches 46; Conservative 31; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLEEMDDEE-----VKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRDLEFLKOLESSDLLDLFEVLVFGK-DGEKRHNEKLTSSIEYKRHGDDYAKYAERIAEE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                         SEQUENCE FROM N.A.
Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan X., Farmer A.,
"Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=1009¢;
                                    SEQUENCE FROM N.A.

KOCZAR D., Reimer T., Rump A., Merck-Rousseau M.F., Rosenthal
Friese K., Thiesen H.J.;

"Role of the BC-2 gene in breast cancer (in preparation).";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                   7.7%; Score 99; DB 4; Length 222;
21.4%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
                                                                                                                                                 Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 Obar R.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                      PFam; PF03357; SNF7; 1.
SEQUENCE 222 AA; 25104 MW; F2B&6C623829E32E CRC64;
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01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-07N-2003 (TrEMBLrel. 24, Last annotation update)
1500016111Rik protein (RIKEN oDNA 1500016L11 gene).
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; ZISSUE-Cerebellum;
MEDLINE-21085660; PubMed=112.7851;
MEDLINE-21085660; PubMed=1827851;
                                                                                                                                                                                                                                                                                                                    EMBL; BC002502; AAH02502.1; -. EMBL; BC047005; AAH47005.1; -. EMBL; BT007298; AAP35962.1; -.
                                                                                                                                                                                                                                                                                        EMBL; AF042384; AAC00005.1; -. EMBL; AJ277113; CAC14310.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                21.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Brain, and Skin;
Slater C., Thill G., Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 39; Conserv
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Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Nagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garziboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Soya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wanshelma Horis R., Kawaji H., Kohtsuki S.,
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:|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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InterPro; IPR005024; DUF279.
Pfam; PF03357; SNF7; 1.
SEQUENCE 222 AA; 25134 MW; F2B86C623832E29E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Breast tumor;
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Search completed: July 5, 2004, 03:12:04
Job time : 29 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5, 2004, 03:07:28 ; Search time 16 Seconds (without alignments) 816.336 Million cell updates/sec
protein search, using sw model
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1 MAYKYDRDLEFLKQLESSDL.....LRLKTQQANGDKKSLQIESI 253
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Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Issued Patents AA:\*

1. / GGTZ 6/ptodata/2/iaa/5A\_COMB.pep:\*

2. / GGTZ 6/ptodata/2/iaa/5B\_COMB.pep:\*

3. / CGTZ 6/ptodata/2/iaa/6A\_COMB.pep:\*

4. / CGTZ 6/ptodata/2/iaa/6B\_COMB.pep:\*

5. / CGTZ 6/ptodata/2/iaa/PGTUS COMB.pep:\*

isting first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	, ,	% Query	, , ,	Ę.	SUMMARIES	Description	
I SO	SCORE	MALCII		9			
ed	9	28.5	273	4,	-09-252-991A-2984		_
7		Ľ,	321	4	US-09-252-991A-29840		_
e	N	19.3	258	4	US-09-489-039A-8852		ď
4	100	7.8	739	4	US-09-543-681A-6437	6437	Æ,
IJ	99		222	m	08-944-604-16	16,	럱
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7	96	7.5	173	N	US-08-658-639-12	12,	냂
8	96	7.5	133	m	-08-944-604-1		ස
σ	95	7.4	2125	4	US-09-919-172-29	29,	낹
10	91.5	7.2	1086	4	US-09-543-681A-7696	7696,	4
11	89,5	7.0		4	-60-	749, A	j.
12	89.5	7.0		4	28-352-584	5845,	Α,
13	89.5	7.0		4			ద
14	89.5	7.0		4	45-236B-	121,	Ä.
15	89.5	7.0		4	US-09-446-301A-50	50	쑶
16	88.5	9.9		4	US-09-446-301A-4	4	72
17	88.5	6.9		4	US-09-099-932-4	Sequence 4, Appl	ፌ
18	00	6.9		4	US-09-489-039A-13363	**	
19	87.5	6.8	732	7	8	Seguence 18, Apr	ద
20		6.8		7	9-307	4	a
21	87.5	6.8		4	US-09-183-861-18	18	ద
22	87.5	6.9	732	4	US-09-022-765-18	18	겁
23	87.5	6.8	732	4	ᅻ	18	ď
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25	87.5	6.8	732	44	US-09-639-206A-18	ednence 18	ద
26	87.5		732	4	-923-	ednence 18	ď
27	87	6.8	491	m	US-09-029-267-2	Sequence 2, App	Δ.

4 US-09-134-001C-3626 Sequence 3625, Ap	4 US-08-637-670-27 Sequence 27, Appl	Sequence 1	4 US-09-107-532A-7062 Sequence 7062, Ap	Sequence 8,	3 US-08-727-616A-8 Sequence 8, Appli	Sequence 8,	Sequence 2,	Sequence 2,	Sequence 7,		Sequence	65 Sequence	362 Sequence	Sequence 7, A	4 US-09-919-901-14 Sequence 14, Appl	4 US-09-919-901-21 Sequence 21, Appl	1100
331	528	691	492	264	264	264	286	286	286	286	286	286	286	286	286	286	
8.9	9.9	9.0	9.9	9	6.5	6.5	6.5	6.5	9.5	6.5	6.5	6.5	6.5	9.1	6.5	5.5	
86.5	84.5	84.5	84	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	83.5	
28	58	00	31	32	33	3.4	35	36	37	38	33	Q.	41	42	43	44	

## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA, FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196,136
FILE REFERENCE: 107196,136
FILE REFERENCE: 107196,136
FRICK APPLICATION NUMBER: US 60/074,788
FRICK APPLICATION NUMBER: US 60/094,190
FRICK APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 QLLERVSNDDLEPLVEYIL-----KARTESLSKQVDFKRMHPEHRRYASAILDELRIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KEMCDEL-----SIKNTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 364; DB 4;
; Pred. No. 1.1e-30;
49; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29840, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AM
                 Sequence 29841, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORGANISM: Pseudomonas aeruginosa US-09-252-991A-29841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.5%;
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US-09-252-991A-29840
US-09-252-991A-29841
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Rubenfield et al. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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APPLICANT GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             566 VLFVAATALSFVIGPAM---KGISDAVNKISNQQIRQILKKVINDGLEAVLGKMIKDIII 622
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--LGGPLGAALNSVKA---VSGSAYRVTIPAVLHI 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 100; DB 4; Length 739;
25.6%; Pred. No. 0.089;
tive 42; Mismatches 65; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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125 High St.
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APPLICANT: KEESEE SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WI, YING-UYE
TITLE OF INVENTION: MATERIALS AND ME
TITLE OF INVENTION: HREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibea
                                                                                                                                                                                                                      ; Sequence 6437, Application US/09543681A; Patent No. 6605709
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187 RTHAAVSVIGHGLVRGAG-
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Best Local Similarity 25.61
Matches 54; Conservative
                                                                       232 ATLRLKTQ 239
                                                                                                                 235 ACLROMIO 242
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ZIP: 02110
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US-09-543-681A-6437
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STATE: MA
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,C39A
CURRENT FILING DATE: 1000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 SWNKLNAEQKAQFLAAVBCRSHELDS:AAHLBRHKKLSEGVILLL-----DERLTAIL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 RIABELQYYGSNSFASFIK-GEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 RSLEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILGRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLK 237
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         AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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; Pred. No. 1.1e-28;
42; Mismatches 112;
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Pred. No. 3.4e-18;
    TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC
FILE REFERENCE: 107196.136
CURRENT PELICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Patent No. 6610836
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ORGANISM: Klebsiella pneumoniae
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1 Similarity 34.3%;
82; Conservative 42
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Best Local Similarity 28.22
Best Local Options 28.22
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Best Local Similarity
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                                                                                                              161 G---RLVDIITAVLAGTI---GYLVV--BILDRKLHAQFIPEFIGSLVIGI---ISVIG 208
106 TLIEGNWLSKILERSLE-EMDDEEVKEMCDELSI-KNTDNLNRQALSA---ATLTLFKMG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 SNSFASFIKG----EGVLYKBILCDVCDKLKVNYNKKTETTLIEONMLSKILERSLEEMD
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OBAK, ROBERT
APPLICANT: WI, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
SADDRESSER: Testa, Furwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.5%; Score 96; DB 2; Length 173;
Best Local Similarity 23.3%; Pred. No. 0.027;
Matches 27; Conservative 33; Mismatches 46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REPERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                   209 HAF----VPSGDLATILIAAV 225
                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08658639; Patent No. 5914238; GENERAL INFORMATION:
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US-08-944-604-12
; Sequence 12, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
                                                                                                                                                                          219 PAYRUTIP----ACIVUATL 234
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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amino acid
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MEDIUM TYPE: Floppy
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: BPIDERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT PAPLICATION NUMBER: 1899-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 DREROKLETQEKKIIADIKKMAKQGQMDAVRIMAKDLVRTRRYVRKEVLMRANIQAVSLK 89
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.7%; Score 99; DB 3; Length 222; Best Local Similarity 21.4%; Pred. No. 0.018; Matches 39; Conservative 48; Mismatches 83; Indels
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                                                                                  NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
RECISTRATION NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
INFORMATION FOR SEC ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7%; Score 99; DB 4; 23.8%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5279, Application US/09134001C Patent No. 6380370
    US/08/944,604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus epidermidis US-09-134-0012-5279
                         FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
                                                                                                                                                                                                                                                                  LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.8%
Marches 62; Conservative
                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-944-604-16
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNYNNDL
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US-09-134-001C-5279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5279
LENGTH: 274
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Query Match 7.4*; Score 95; DB 4
Best Local Similarity 25.4*; Pred. No. 1.5;
Matches 46; Conservative 35; Mismatches
           Score 95;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     817 -----
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US-09-543-681A-7696
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US-09-198-452A-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 NNSMAQAMKGVTKAMGTMNRQLKLPQIQKIMMEFERQAEIMDMKEEMMNDAIDDAMGDEE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 DEE-----VXEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.3%; Pred. No. 0.027;
Matches 27; Conservative 33; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. 6673545 3774181CD1
US-03-919-172-29
                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT. INPORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REPERBUCK/OCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGram
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09919172
Patent No. 6673545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELBEAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 173 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                         STATE: MA
COUNTRY:
ZIP: 0213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-944-604-12
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GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
TITLE OF INVENTION: Chlamydia and uses thereof, in particular for the diagnosis, pr
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NOS: 8344
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                                                                                                                                                                                986 SFRDEKELERLŐICÓRKSDHLKEQFEKSHEQLLONIKAEKENNDKIORLNEELEKSNECA 1045
                                                                                                                                                                                                                                                                                                                                                                                                    63 EELQYYGSNSFASFIKGEGYLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            861 KGDEWAGLKQGLSDFSESAMDVMENVTTNALMNMSDALADFALTGKGSFKDFANAVI 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YKYDRDLEFLKOLESSDLLDLFEVLVPGKDGEKRHNEKLTSSIEYKRHGDDYAKYAERIA 62
                                                                                                                 2 AYKYDRDLEFLK--QLESSDLLDLF----EVLVFGKDGEKRHNEKLTSSIEYKRHGDDYA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 EMD------DEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVI
                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 91.5; DB 4; Length 1086; Best Local Similarity 19.5%; Pred. No. 1.3; Matches 43; Conservative 38; Mismatches 73; Indels 67
                                                                                                                                                                                                                                                                                                                                                                    98 -NYNKKTETTLIEQNMLSKI--LERSLEEMDD--EEVKEMCDELSI----
DB 4; Length 2125;
                                                                                                                                                                                                                                            56 KYAERIAEEL--QYYGSNSFASFIKGEG---VLYKEILCDVCDKLKV--
                                                            62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDITENTANGENTIFKALEAGG-----QAMGF---DMGWMSKG 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7696, Application US/09543681A Patent No. 6605709
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APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: White, Albert H.
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004, and Methods for Control of Invertebrates
FILE REFERENCE: 1992.006-30
UNRENT APPLICATION NUMBER: US/09/345, 236B
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 96
LENGTH: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan B.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 2004, 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 CDELSIKNTDNLN----RQALSAATLILFKMG---GFKSYCLAVIVANAVAKTILGRGLS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 PENLNDIITDQLRDFMAQELKKAAENYVPKWGSTVGESKSALAITVADRVSRSFWYEGRI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 VFEVVGGGPEGDYAAGEEDBVSRNSINFDMASEVQSTDAAKVMELFSALSEEQRNVILMN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 FASFIKGEGULYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERSLEEMDDEEVKEM 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTRILSFLIGPVGWII------TGVWTAIDIAGPAYRVTIPA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LFEVIAFGKDGEKRHNEK-----LITSSIEYKRHGDDYAKYAE---RIAEELQYYGSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 89.5; DB 4; Best Local Similarity 23.5%; Pred. No. 0.75; Matches 60; Conservative 34; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121, Application US/09345236B
Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Beenel, James J.
                                                             ; Sequence 98, Application US/09345236B
; Patent No. 6521454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mosquito baculovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: mosquito baculovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 FGAAPSGSGT-----
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                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Tukto, Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tukuo, Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 LAGNOV--
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US-09-345-236B-121
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US-09-328-352-5845
US-09-328-352-5845

Sequence 5845, Application US/09328352

Patent No. 656258

GENERAL INFCRMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA.

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-66-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 SLAGN--QVLTRTLSFLTG-----PVGWIITGVWTAIDIAGPAYRVTIPACIVVATL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 DSRDVKVPSLEGKÇTRQEKTTSSKGNTRTESRKFADBEKRVDDEIAEVGSKEREGESQES 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 DLFEVLVFGKDGEKRHNEKLISS----ISYKRHGDDYAKYAERIAE-
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CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 6849 LENGTH: 282 LENGTH: 282
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ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                  ORGANISM: Chlamydia pneumoniae
US-09-198-452A-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKTQQANGDKKSLQ 249
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US-09-328-352-5845
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Sequence 50, Application US/09446301A
Fatent No. 650693
GENERAL INFORMATION:
APPLICANT: EL SCH, NEVINE
APPLICANT: EL SCH, NEVINE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
FILE REPERENCE: 03715-0059
CURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT PILING DACE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SSQ ID NO 50
LENGTH: 560
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                                                                                                        73 FASFIKGEGVLYKEILCDVCDKLXVNYNKKTETTLIEQNALSKILERSLEEMDDEEVKEM 132
                                                                                                                                                                                     133 CDELSIKNTDNIN----RQALSAATLTLFKMG---GFKSYQLAVIVANAVAKTILGRGLS 185
                                                                                                                                                                                                                                                                  243 PENLNDIITDQLRDFMAQELKKAAENYVPKWGSTVGESKSALAITVADRVSRSFWYEGRI 302
                                                                                                                                                                                                                                                                                                                                               68 YGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKK--TETTLIEQNMLSKILERSLEEMD 125
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                                                                               23 LFEVLVFGKDGEKRHNEK-----LTSSIEYKRHGDDYAKYAE---RIAEELQYYGSNS 72
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                                       92; Indels 69; Gaps
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7.0%; Score 89.5; DB 4; Length 560;
Best Local Similarity 25.3%; Pred. No. 0.78;
Matches 37; Conservative 31; Mismatches 47; Indels 31
  Length 546;
Query Match
7.0%; Score 89.5; DB 4;
Best Local Similarity 23.5%; Pred. No. 0.75;
Matches 60; Conservative 34; Mismatches 92;
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                                                                                                                                                                                                   213 FGAAPSGSGT----
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US-09-446-301A-50
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	Score	Query Match	Length	DB	ID	Description
	1279	100.0	253	5	AAE26860	Aae26860 Helicobac
7	1279	100.0	265	ιΩ	AAE26878	Aae26878 Helicobac
m	1270	99.3	253	N	AAW20486	Aaw20486 H. pylori
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Ŋ	1270	99.3	256	N	AAW20866	Aaw20866 H. pylori
ø	1264	98.8	253	Ŋ	AAE26880	Aae26880 Helicobac
7	1264	98.86	265	'n	AAE26879	Aae26879 Helicobac
80	472.5	36.9	155	N	AAW98774	Aaw98774 H. pylori
σ	252	19.7	4,	Ŋ	AAE26876	Aae26876 Helicobac
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12	152	11.9	3.0	'n	AAE26874	Aae26874 Helicobac
13	150	11.7	30	'n	AAE26872	Aae26872 Helicobac
14	66	7.7	222	4	AAB98720	Aab98720 Human bre
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19	96.5	7.5	701	Ŋ	ABP73563	Abp73563 Candida a
20	96	7.5	173	N	AAW44365	Aaw44365 Breast ca
27	96	7.5	173	4	AAB98717	Aab98717 Human bre
22	95	7.4	517	9	ABU26619	Abu26619 Protein e
23	iń Gi	7.4	2125	Ŋ	ABG77172	Abg77172 Prostate
24	iń) Øv	7.4	2649	7	ADB79929	Adb79929 Human put
25	93.5	7.3	1196	9	ABU24813	Abu24813 Protein e

Aag82981 S. epider	Abu19293 Protein e	Aau33755 Staphyloc	Aau36548 Staphyloc	Abp30227 Streptoco	Abp28162 Streptoco	Aag44550 Arabidops	Aag48726 Arabidops	Aag44549 Arabidops	Aag48725 Arabidops	Aag48724 Arabidops	Aag44548 Arabidops	Abp30479 Streptoco	Abp27884 Streptoco	Abr52974 Protein s	Aay51631 M. jannas	Aay52002 M. jannas	Aay31948 Plasmodiu	Aay31947 Plasmodiu	Aag82765 S. epider
AAG82981	ABU19293	AAU33755	AAU36548	ABP30227	ABP28162	AAG44550	AAG48726	AAG44549	AAG48725	AAG48724	AAG44548	ABP30479	ABP27884	ABR52974	AAY51631	AAY52002	AAY31948	AAY31947	AAG82765
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# ALIGNMENTS

The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrilis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is the proteins, useful as vaccines for raising immune response in animals. HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis, antihinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer. proteins, HP30 and HP56, and nucleic acids encoding Claim 1; Page 111-112; 127pp; English. AAE26860 standard; protein; 253 AA Jackson WJ; Helicobacter sp. HP30 protein. 87-DEC-2001; 2001WO-US048392. 07-DEC-2000; 2000US-00732091. (ANTE-) ANTEX BIOLOGICS INC. (first entry) WPI; 2002-666854/71. Tian J, Walker R, Movel Helicobacter N-PSDB; AAD44513. Helicobacter sp. WO200251237-A2. 13-DEC-2002 04-JUL-2002. AAE26860; RESULT 1 

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AAE2687 RESULT

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disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                 133 LEEMDDEEVKEMCDELSIKUTDNINRQALSAATITLFRMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 GRGLSLAGNQVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRKTQQ
                                                                                                                                                                                                                                                                                                                 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                                                                                                                                                                                                    Length 265;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                      100.0%; Score 1279; DB 5;
100.0%; Pred. No. 1.9e-118;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW20486 standard; protein; 253 AA.
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                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                  Sequence 265 AA;
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01-APR-1996;
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il as vaccines for raising immune response in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                      1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
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                                                                                  100.0%; Score 1279; DB 5; 100.0%; Pred. No. 1.8e-118;
                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by TTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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              Helicobacter sp. HP30 protein
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                                                                                Query Match
Best Local Similarity 100.
Matches 253; Conservative
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N-PSDB; AAD44535.
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                                                  AA;
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                                                  Sequence 253
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N-PSDB; AAT77491
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                   The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ArCC 55679) was determined from overlapping contigs generated by rechanically shearing the bacterial DNA. The sequences were analysed for OFF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; artisense;
                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                Length 253;
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                                                                                                                                                                                                                99.3%; Score 1270; DB 2; 99.2%; Pred. No. 1.4e-117; ive 1; Mismatches 1;
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 Page 651; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW24673 standard; protein; 253 AA.
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                                                                                                                                                                                                                                         Conservative
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This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for acid sequences, and corresponding proteins, are also useful for meleic acid sequences for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA care blunt-ended and ligated to unique BstXI-linker adapters in 100-1000 fold molar excess. These linkers are complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate tiself easily. The linker-adapter inserts were ligated to each of the 20 pWPX vectors to construct a series of shotgun subclone libraries. The number for this sequence was obtained from the related specification,
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Helicobacter pylori nucleic acid sequences and related proteins - used for diagnostics and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
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                                                                                                                 Claim 18; Page 184; 235pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ANEDKKSLOIESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-1997
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B asatritus, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP30 plasmid DNA encoded protein
                                                                                                                                                                                                                                                                                                                                                                          Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 JARBIQYYGSNSPASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGLSLAGNOVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ
           low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.8%; Score 1264; DB 5; 98.8%; Pred, No. 5.6e-117; ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 126-127; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE26879 standard; protein; 265 AA.
                                                                                                                                                                              07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                   (ANTE-) ANTEX BIOLOGICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ANEDKKSLQIESI
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                                                                                                                                                                                                                                                                                                                        WPI; 2002-666854/71.
                                                                                                                                                                                                                                                                                      Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        N-PSDE; AAD44537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 253 A.B.;
                                                                      Helicobacter sp
                                                                                                         WO200251237-A2.
                                                                                                                                           04-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                      Tian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori infe cycle activators or inhibitors. The genomic sequence of H. pylori (ARCC 5679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGLSLAGNOVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HP30; HP56; immune response; therapy; Helicobacter infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IABELOYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQUMLSKILERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGLSLAGNOVLTRILSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRIKTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IABELOYYGSNSPASFIKGEGVLYKBILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
                                                                                                                                                                                                                                                                    Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No. 1.5e-117;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter sp. pQE/HP30 plasmid DNA encoded protein.
                                                                                                                                                                                  BL;
                                                                                                                                                                                                                                                                                                                                            Claim 61; Page 1269; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE26880 standard; protein; 253 AA.
                                                                                                                                                                                  Mellgaerd
                                                                                           95US-00487032.
96US-00630405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%;
                                                         96WO-US009122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.2:
Matches 251; Conservative
                                                                                                                                                                                  or,
                                                                                                                                                                                  Berglindh
                                                                                                                                                                                                                   WPI; 1997-052306/05.
                                                                                                                                               (ASTR ) ASTRA AB.
                                                                                                                                                                                                                                      N-PSDB; AAT68119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 256 AA;
                                                                                           07-JUN-1995;
                                                                                                           01-APR-1996;
                                                         06-JUN-1996;
                      19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE26880;
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                                                                                                                                                                                  Smith D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
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Length 253; Indels 9 9 120 120 240

04-JUL-2002

E530;

Tian J,

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invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and ducdenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis
                                                                                                                           GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynuclectides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 NEKLISSIEYKRHGDDYAKYABRIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a Helicobacter pylori GHPO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.9%; Score 472.5; DB 2 63.3%; Pred. No. 1.3e-38; iive 22; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 1676-1677; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE26876 standard; peptide; 49
                                                                                                                                                                                                                                                                                                                        98WO-US006371.
                                                                                                                                                                                                                                                                                                                                                                97US-00833457.
                                                                                                                                                                                                                                                                                                                                                                                                       97US-00902615.
                                                                                                                                                                                                                                                                                                                                                                                      97US-00881227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Al-Garawi A,
                                                                                             H. pylori GHPO 1170 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-542293/46.
N-PSDB; AAX14493.
                                                                                                                                                                                                 Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kleanthous H,
                                                                                                                                                                                                                                                                                                                        01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1997;
                                                                                                                                                                                                                                         W09843478-A1
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                                                         31-MAR-1999
                                                                                                                                                                                                                                                                                  08-OCT-1998
                 AAW98774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventor is useful for producing an immune response. It is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with a felicobacter. Fharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcars, gastric cancers such as adenocarcinose, and low grade B cell Immedical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HPS6 plasmid DNA encoded protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 LEEMDDEEVKEMCDELSIKNTDNLNRQALSAATLTLFRØGGFKSYQLAVIVANAVAKTIL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                          type B gastritis, antiînflammatory; adenocarcinoma, defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGLSLAGDQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRKTQQ
                                                         Helicobacter infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 6e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                 Helicobacter sp. pQE/HPS6 plasmid DNA encoded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 124-125; 127pp; English
                                                         HP56; immune response; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                             Jackson WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.8%;
                                                                                                                                                                                                                                                                                                                            07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                                                    07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                                                                                                                                                                (ANTE-) ANTEX BIOLOGICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 250; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD44536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 265 AA;
                                                                                                                                                           Helicobacter sp.
                                                                                                                                                                                                   WO200251237-A2
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Oomen RP;

Tomb J,

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NYNKKTETTLIEGNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NROALSAATL 154
                                                             Helicobacter sp. HP30-derived peptide #5.
                                                                                                                         TLFKWGGFKSYQLAVIVANAVAKTILG 181
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AAW98774 standard; protein; 155 AA.

RESULT 8
AAW98774
ID AAW98

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181

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Gaps

3,

Indels

29; DB 2;

Length 155;

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Walker R,
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                                                                                                                                 N-PSDB; AAD44526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38 AA;
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                                                                                Tian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
             type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
response; therapy; Helicobacter infection; vaccine;
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Pred. No. 2e-17;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.7%; Scor.
100.0%; Pred. No. zc.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 116, 127pp; English.
                                                                                                                                                                                                                                                                                   Jackson WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE26873 standard; peptide; 38
                                                                                                                                                                                  07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                   07-DEC-2000; 2000US-00732091.
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Best Local Similarity 100.8
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                   WPI; 2002-666854/71.
N-PSDB; AAD44529.
                                                                                                                                                                                                                                                                                   Walker R,
                                                                                Helicobacter sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49 AA;
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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the proteins, useful as vaccines for raising immune response in animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.5%; Score 198; DB 5; I 100.0%; Pred. No. 3.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 DYAKYAERIABELQYYGSNSPASFIKGEGVLYKEILCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 115; 127pp; English.
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07-DEC-2000; 2000US-00732091.
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Claim 7; 

invention relates to Helicobacter HP30 or HP56 polypeptide and Page 116; 127pp; English.

Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating disorder or disease associated with infection of an animal with

Sequence 41 AA;

Gaps ö 15.2%; Score 194; DB 5; Length 41; 100.0%; Pred. No. 8.9e-12; tive 0; Mistatches 0; Indels Conservative Local Similarity 4 Query Match Matches

145 NRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTILGRGLS 185 NRQALSAATLTLFK%GGFKSYQLAVIVANAVAKTILGRGLS

RESULT 12 AAE26874

AAE26874 standard; peptide; 30 AA AAE26874;

(first entry) 13-DEC-2002 Helicobacter sp. HP30-derived peptide #3.

HP30; HF56; immune response; therapy; Helicobacter infection; vaccine; type B gastritus; antihalmmatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer. 

Helicobacter sp.

WO200251237-A2

C4-JUL-2002

07-DEC-2001; 2001WO-US048392.

07-DEC-2000; 2000US-00732091.

(ANTE-) ANTEX BIOLOGICS INC

Jackson WJ Walker R, Tian J,

WPI; 2002-666854/71 N-PSDB; AAD44527 Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.

Claim 7; Page 115; 127pp; English.

Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating disorder or disease associated with infection of an animal with

ìs on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence Helicobacter sp. HP30-derived peptide ឧឧឧ

Sequence 30 AA;

Gaps . 0 Length 30; Indels Score 152; DB 5; I Pred, No. 8.5e-08; 11.9%; Scor. 100.0%; Pred. No. c. ... 0; Mismatches Query Match
Best Local Similarity 100.
Matches 30, Conservative

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121 LEEMDDREVKEMCDELSIKNTDNLNRQALS 150 1 LEEMDDEEVKEMCDELSIKNTDNLNRQALS à 셤

AAE26872 standard; peptide; 30 AA

AAE26872;

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(first entry) 13-DEC-2002 Helicobacter sp. HP30-derived peptide #1.

HP30; HP56; immune response; therapy, Helicobacter infection, vaccine; type B gastritis, antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.

Helicobacter sp.

WO200251237-A2.

04-JUL-2002.

07-DEC-2001; 2001WO-USD48392

07-DEC-2000; 2000US-00732091.

(ANTE-) ANTEX BIOLOGICS INC.

Jackson WJ;

Walker R,

Tian J,

WPI; 2002-666854/71. N-PSDB; AAD44525.

Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.

Claim 7; Page 115; 127pp; English

The invention relates to Helicobacter HPDO or HPDE polypeptide and immune response. It is useful for preventing, treating or ameliorating an disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastrifis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as bost defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide 

Sequence 30 AA;

ò Length 30; Indels Score 150; DB 5; 1 Pred. No. 1.3e-07; ö Mismatches 11.7%; Sco... 100.0%; Pre Conservative Similarity Mar. Local Sim. 30; Query Match Matches

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Gaps

1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFG 30

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**AAB98**"

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SLEEMDDEE-----VKEMCDELSIKNTDNLNRQALSAATLTLFKMGGFKSYQLAVIVANA 174
                                                                                    150 AMGDEEDEEBSDAVVSQVLDELGLSLTDELSNLPSTGGSLSV-AAGGKKAEAAASALADA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5279.
                                                                                                                                                                                                                                                                                        ABP40434 standard; protein; 274 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
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                                                                                                                                              175 VA 176
                                                                                                                                                                                      DA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and their use inventors insured numers of cancer associated proteins, and their use in diagnosing and detecting breast cancer associated proteins of the invention are nuclear matrix proteins designated BC-2 (AAB98722), although 6 other breast cancer-associated isoform 8 (BC-8B, AAB98722) and CC BC-8 isoform 8 (BC-8B, AAB98722), although 6 other breast cancer-associated conclear matrix proteins (BC-1, BC-3, BC-4, BC-5, BC-6, and BC-7) were also isolated (sequences not given in the specification). The novel breast cancer calls, but are not present in the nuclear matrix of chem normal breast tissue. The invention also encompasses fragments of from normal breast cancer diagnosis. The breast cancer matrix of proteins of the invention or fragments thereof may be detected in a sample of breast cancer diagnosis. The breast cancer marker cancer diagnose breast cancer diagnosis and detected in a sample of breast cancer. Nucleic acids encoding the breast cancer. Nucleic acids encoding the breast cancer associated proteins may also be used to prepare antibodies, particularly monoclonal antibodies, which may be used to detect or diagnose breast cancer. Nucleic acids encoding the breast cancer associated proteins may also be used in the diagnosis and detection of breast cancer, and in the isolation of DNA or protein sequences which may increase cancer associated proteins. The present sequence represents the full-length breast cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to novel human breast cancer-associated proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing or detecting breast cancer in an individual comprise detecting the presence of breast cancer-associated proteins in
                                                                                                                                                                                                                                                                    Human breast cancer-associated protein; BC-2; marker protein; nuclear matrix protein; diagnosis; detection; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 222;
                                                                                                                                                                                                                              Human breast cancer-associated protein BC-2, SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.7%; Score 99; DB 421.4%; Pred. No. 0.27 tive 48; Mismatches
          MAYKYDRDLEFLKQLESSDLLDLFEVLVFG 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 27-30; 30pp; English.
                                                                                                            AAB98720 standard; protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00944604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00658639
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H
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Best Local Similarity 21.4<sup>5</sup>
Matches 39; Conservative
                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MATR-) MATRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-396355/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obar R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH25902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein BC-2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            US6218131-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detecting t
biological
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                                                                                                                                                                 ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 SGAEĞIRVEDIMARIATKLGYPESNSFVINIVIEPVLHNEAYPRL------YRIKIRDI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 YKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKVNYNKKT-ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 99; DB 5; Length 274;
13.8%; Pred. No. 0.37;
.ve 44; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSS--
                                                                                                              Disclosure, SEQ ID NO 5279; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%;
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LQYYGS-NSFASFIKG----EGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILER 119 | | | : | : | : | : | : : : | : : : : | DRERQKLETQEKKILADIKKWAKQGQMDAVRIMAKDLWRTRRYVRKFVLMRANIQAVSLK 89 DRDLBFLKQLESSDLLDLFEVLVFCK-DGEKRHNEKLTSSIEYKRHGDDYAXYAERIAEE 64

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Oy 106 TLIEQUMLSKILERSLE-EMDDEEVEMCDELSI-KNTDNINRQALSA---ATLILEFWG 160

DD 101 NLIKISOANEISRQITNGTMTLEEAKYQLEEITVAKRDSSLPFKGIAAAIIATSFLYLGG 160

QY 161 GFKSYQLAVIVANAVAKTILGRGISLAGNQVLTRIL-SFLTGPVGWIITGVWTAIDIAG 218

DD 219 PAYRVIIE---ACIVVTL 234

DD 209 HAF---VPSGDLATIIIAAV 225
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Search completed: July 5, 2004, 03:11:25 Job time : 40 secs us-09-732-091-4.rpr

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version 5.1.6
- 2004 Compugen Ltd.
GenCore
Copyright (c) 1993
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model ŝ protein search, using OM protein 5, 2004, 03:10:43 ; Search time 14 Seconds (without alignments) 1738.318 Million cell updates/sec July Run on:

US-09-732-091-4 1279 Title: Perfect so Sequence:

......LRLKTQQANGDKKSLQIESI 253 1 MAYKYDRDLEFLKQLESSDL. score:

BLOSUM62 Gapcp 10.0 Scoring table:

, Gapext 0.5

of hits satisfying chosen parameters: Total number

283366 seqs, 96191526 residues

Searched:

seg length: 0 seg length: 2000000000 Minimum DB : Maximum DB :

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Ouerv				
No.	Score	Match	Length	DB	D	Description
1	1279	100.0		7		conserved hypothet
7	1270	99.3		~	B71800	hypothetical prote
m	784.5	61.3	207	~	E64718	conserved hypothet
4	630	49.3		ď	A71800	hypothetical prote
5	472.5	36.9		~	C64718	conserved hypothet
9	265	20.7		N	C64.721	hypothetical prote
r-	265	20.7	237	7	AC0503	conserved hypothet
60)	262	20,5	237	N	089063	probable oxidoredu
σ	262	20.5	237	N	C85481	probable oxidoredu
10	133	10.4	39	7	F64718	hypothetical prote
11	98.5	7.7	1009	C)	C89910	hypothetical prote
12	98	7.7	282	Ġ	AE0360	
13	96	7.7	1099	¢ή	G90546	conserved hypothet
7.4	97.5	7.6	H H M	C)	C81380	probable D-2-hydro
15	97.5	7.6	728	Ćή	A81385	probable ATP /GTP
16	97	7.6	916	Ċ	E71330	probable preprotei
17	96.5	7.5	373	Cή	G70355	8-amino-7-oxononan
18	96	7.5		7	T33071	hypothetical prote
13	96	7.5	4	63	F96920	probable permease
20	95.5	7.5	344	CI	A47025	abortive phage res
21	95	7.4	G	Cł	C81327	hypothetical prote
22	95	7.4	2649	7	A40937	bullous pemphigoid
23	93.5	7.3		Ŋ	S49252	penicillin amidase
24	93	7.3	355	7	E90488	transposase ISC122
25	93	7.3	610	7	G70178	exodeoxyribonuclea
26	92.5	7.2	430	7	T33070	hypothetical prote
27	92.5	7.2	802	7	I39665	E
28	92.5	7.2	886	7	T16536	
29	92	7.2	308	~	H81345	

repeat organellar	RNA polymerase sig	PET112 homolog - M	hypothetical prote	rad 26 protein - f	probable membrane	replication factor	body-wall muscle t	hypothetical prote	hypothetical prote	vsaa-like (mycopla	hypothetical prcte	hypothetical prote	ribonucleoprotein	conserved hypothet	CT671 hypothetical
T18372	G72253	A64320	T24622	S42797	S53378	E64477	A45488	A12368	B97214	D90550	T18417	T18418	503849	A72046	F86578
~	2	7	~	~	N	2	7	N	7	7	7	7	-	7	7
1939	399	472	508	615	1769	1847	284	35.9	320	1017	1411	1417	404	280	280
7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.1	7.1	7.1	7.1	7.1	7.0	7.0	7.0
92	91.5	91.5	91.5	91.5	91.5	91.5	91	91	90.5	90.5	90.5	90.5	90	89.5	89.5

RESULT 1 D64718 Conserved hypothetical protein HP1588 - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999 C;Accession: D64718 R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKerson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Aguine 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Accession: D64718
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-253 < TOM>
A.Residues: 1-253 < TOM>
A.Cross-references: GB:AE000656; GB:AE000511; NID:g2314771; PIDN:AAD08627.1; PID:g2314

Query Match 100.0%; Score 1279; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 4e-88; Matches 253; Conservative 0; Mismatches 0; Indels 0

1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER 60 09 1 MAYKYDRDLEFLKQLESSDLLDLFEVLVFGKDGEKRHNEKLTSSIEYKRHGDDYAKYAER ద à

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Gaps

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120 61 IARELQYYGSNSFASFIKGBGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS 120 61 IARELQYYGSNSPASFIKGEGVLYKEILCDVCDKLKVNYNKKTETTLIEQNMLSKILERS g ð.

121 LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLTLFKMGGFKSYQLAVIVANAVAKTIL 180 181 GRGLSLAGNQVLTRTLSFLTGPVGWIITGVWTAIDIAGPAYRVTIPACIVVATLRLKTQQ 셤 à

240

LEEMDDEEVKEMCDELSIKNTDNINRQALSAATLITEKMGGFKSYQLAVIVANAVAKTIL 180

121

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# RESULT 2

B71800

hypothetical protein jhp1494 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999
C;Accession: B71800
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R

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hypothetical protein jhp1493 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: A71800
C;Accession: A71800
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. R;Alm, R.A.; Ling, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Helicobacter pylori
Cispecies: Op-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cispecies: Op-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
Cispecies: Op-Aug-1997 #sequence, A.R.; Clayton, R.A.; Kaclak, H.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.J.; Kallak, H.G.; Bowman, C.; Watthey, Nature 188, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A.Reference number: A64520; MUID:97394467; PMID:9252185
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Residues: L.SS crows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE001439; NID:94156120; PIDN:AAD07072.1; PID:9415
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                                121 GPKSYQLALIVANAVIKAIFQRGLSLGANAALTRGLSILTGPIGWIITGVWTAIDIAGPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 NYNERSATSLIEQNMLSKLLKDSLEROSGREIKELCDGLGMPNIDKVIGENKQVLIASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 TLFKMGGFKSYQLAVIVANAVAKTILGRGL-SLAGNQVLTRTLSFLTGPVGWIITGVWTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 NEKLTSSIEYKRHGDDYAKYAERIAEELQYYGSNSFASFIKGEGVLYKEILCDVCDKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 NYNKKTETTLIEQNMLSKILERSLEEMDDEEVKEMCDELSIKNTDNL---NRQALSAATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 59.8%; Pred. No. 7.4e-40;
Matches 122; Conservative 32; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 472.5; DB 2
Pred. No. 2.8e-28;
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63.34; Pred. No. 2...
22; Mismatches
                                                                                                                                     181 YRVTIPACILVATLRLKA-QANEIKNIL 207
                                                                                                  221 YRVTIPACIVVATLRLKTQQANGDKKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 IDIAGPAYRVIIPACIVVATURLK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 INLAGPAYRVTVPACVLVATLRKK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule_type: DNA_
A;Residues: 1-209 <ARN>
A;Cross-references: GB:AE001571; G
A;Experimental source: strain J99
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Best Local Similarity
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ilves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Accession: B71800
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-253 ARN>
A; Residues: 1-253 ARN>
A; Cross-references: GB:AE001571; GB:AE001439; NID:G4156120; PIDN:AAD07073.1; PID:G415612
A; Cross-references: A; Application: Briain J99
C; Genetics: A; Gene: jhp1494
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Ritomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, W.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Mature 388, 539-547, 1997
Mature 388, 539-547, 1997
Millin, E.; Hayes, W.S.; Borodovsky, M.; Karzyk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
M; Reference number: A64520; MUID:97394467; PMID:9252185
M; Accession: E64718
M; Accession: E64718
M; Residues: DNA
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C,Species: Helicobacter pylori
C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
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Post-processing: Minimum Match 0% Maximum Match 100%

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Listing first 45 summaries

Command line parameters: Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aae26860 Helicobac	Aae26878 Helicobac	Aaw20486 H. pylori	Aaw24673 H. pylori	Aaw20866 H. pylori	Aae26880 Helicobac	Aae26879 Helicobac	Aaw98774 H. pylori	Aae26876 Helicobac	Aae26873 Helicobac
SUMMARIES		ID	AAE26860	AAE26878	AAW20486	AAW24673	AAW20866	AAE26880	AAE26879	AAW98774	AAE26876	AAE26873
		Match Length DB	253 5	265 5	253 2	253 2	256 2	253 5	265 5	155 2	49 5	3.0
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# ALIGNMENTS

HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer. AAE26860 standard; protein; 253 AA Jackson WJ; Helicobacter sp. HP30 protein. 07-DEC-2001; 2001WO-US048392. 07-DEC-2000; 2000US-00732091. (ANTE-) ANTEX BIOLOGICS INC. (first entry) WPI; 2002-666854/71. Tian J, Walker R, Helicobacter sp. WO200251237-A2. 04-JUL-2002. 13-DEC-2002 AAE26860; RESULT 1 

Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals. N-PSDB; AAD44513.

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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B agastrils, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. PQE/HP30 protein
Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                                                                                                                                                               HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                       AAE26878 standard; protein; 265
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                                                                                                                                                                                                                        (first entry)
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N-PSDB; AAD44535.
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                                                The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, wirulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30 protein
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Mismatches:
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                                          LeuaspleupheGluValLeuValPheGlyLvsaspGlyGluLysargHlsAsnGluLys
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                                                                                                ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
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The present sequence is a H. pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori infe cycle activators or inhibitors. The genomic sequence of H. pylori (ARCC 5679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of all least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or experted membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts

Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vactimes to treat or prevent H. pylori infection, and to detect Helicobacter.

Mellgaerd

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Berglindh

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Smith

(ASTR ) ASTRA 07-JUN-1995; 01-APR-1996;

WPI; 1997-052306/05. N-PSDB; AAT67811.

95US-00487032 96US-00630405

61; Page 651; 1481pp; English

Claim

ACGGACATITAAACAGACAGCTIAAGCGCGGCGACTITAACGCTGITIAAAAIGGGG TIGGAAGAATGGATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAC LeuThrSerSerIleGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg **ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA** GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA TIGGATITIGITIGAGGIGCITGITITIGGTAAAGACGGCGAAAAAAGACACAAIGAAAAA CTGACCAGCTCCATAGAATACAAAAGGCATGGTGATTACGCTAAATACGCAGAAAGA 61 ŧ4 21 121 41 181 8 101 361 121 427 241 301 셤 쉱 셤 g 임 à 유 à Š ò g ò 8 Š ö

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; ducdenal ulcer disease; chronic gastritis; diagnosis; envelope.

Helicobacter pylori

06-JUN-1996;

19-DEC-1996

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H. pylori cytoplasmic protein, 4095342.aa

(first entry)

29-JJL-1997

Ā

protein; 253

standard;

AAW20486

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Length: Matches: L Mismatches: Indels:

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Sequence 253 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents an H. pylori cytoplasmic protein. Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H. pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of Helicobacter species in a sample. Antisense of a gene from Helicobacter species. H. pylori whole genomic DNA was colared and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique BstXt-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore
                                                                                                                                                                                                                                                                                                                                                              Transmembrane, cytoplasmic; cell envelope, flagella, transport; secreted, periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition.
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 ThrispasnLeuAsnArgGlnAlaLeuSerAlaAlaThrLeuThrLeuPheLysMetGly
                         GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
                                                                                                                   GGTCCTGTTGGCTGGATCATTACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins
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                                                                                                                                                                                                                        AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal
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                                                                                                                                                                                                                                                                                protein; 253
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for diagnostics and
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N-PSDB; AAT77491.
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the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts were ligated to each of the 20 pWFX vectors to construct a series of shogun subclone libraries. The purified DNA samples were then sequenced. Note: The ORF/protein reference number for this sequence was obtained from the related specification,
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Conservative:
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Best Local Similarity:
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RESULT 5

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GGTCCTGTTGGCTGGATCATTACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCT 660
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                                                                                                                                                                                                                                            241 GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC
                                                                                                            ACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGG
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                                ATCGCTGAAGAGTTGCAATACTATGGCAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                 64 IlealaGluGluLeuGlnTyrTyrGlySerAsnSerPheAlaSerPheIleLysGlyGlu
                                                                                                                                                            ttggaagaantggatgaagaagtgaaagaaatgtgcgatgaattatccataaaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-666854/71
N-PSDB; AAD44537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                  Cytoplasmic; vaccine; preventioc; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
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Indels:
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             standard; protein; 256
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96US-00630405.
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N-PSDB; AAT68119.
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Best Local Similarity:
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01-APR-1996;
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Pred. No.:
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                                                     The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcars, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP30 plasmid DNA encoded protein
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    bl Helicobacter proteins, HP30 and HP56, and nucleic acids encoding proteins, useful as vaccines for raising immune response in animals
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Matches:
Conservative:
Mismatches:
                                      Disclosure; Page 126-127; 127pp; English.
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1264.00
99.60%
98.81%
93.70%
          Novel Helicobacter
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Best Local Similarity:
                                                                                                                                                                                                      Sequence 253 AA;
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with the icobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastric tancers such as adenocaccinoma, and low grade B peptic ulcars, gastric cancers such as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. pQE/HP56 plasmid DNA encoded protein
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                                                                                                                                                                                                                                                                                                                                    AAE26879 standard; protein; 265
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97US-00881227
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      29-JUL-1997;
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                                                                              ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA 240
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                             GGTCCTGTTGGCTGGATCATTACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCT
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                                                          LeuThrSerSerLeuGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg
                                                                                     TIGGAAGAAATGGATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAC
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      MetAlaTyrLysTyrAspArgAspLeuGluPheLeuLysGlnLeuGluSerSerAspLeu
                                                                                                                                       GGTTTTAAATCTTATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
protein; Helicobacter infection; gastroduodenal disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                               This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastricis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
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                                                                                                                                                                    New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
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Matches:
Conservative:
Mismatches:
Indels:
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                               (INWR ) MERIEUX ORAVAX PASTEUR MERIEUX
(HUMA-) HUMAN GENOME SCI INC.
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97US-00902615
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63.27$
                                                                                        Al-Garawi A,
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N-PSDB; AAX14493.
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B asstritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel Helicobacter proteins, HP30 and HP56, and nucleic acids encoding the proteins, useful as vaccines for raising immune response in animals.
                                                                                                                                           HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis, antichinflammacory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jackson WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphoma. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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                                                                                                                         HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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Best Local Similarity:
Query Match:
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Helicobacter sp. HP30-derived peptide #3.
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Best Local Similarity:
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                                                                                                                                                       Helicobacter sp.
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                                                                                                                                                                                                                                                                                                                                                                                                               el Helicobacter proteins, HP30 and HP56, and nucleic acids encoding proteins, useful as vaccines for raising immune response in animals.
                                                        E230; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antilufilammatory; adebocarcinoma; defense mechanism; low grade B cell lympioma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                            sp. HP30-derived peptide #4.
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Best Local Similarity:
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                            Helicobacter
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The invention relates to Helicobacter HP30 or HP56 polypeptide and peptides derived from them. The invention is useful for producing an immune response. It is useful for preventing, treating or ameliorating a disorder or disease associated with infection of an animal with Helicobacter. Pharmaceutical composition and vaccines comprising the sequences of the invention is useful for treating type B gastritis, peptic ulcers, gastric cancers such as adenocarcinoma, and low grade B cell lymphona. The invention is useful as reagents for clinical or medical diagnosis of Helicobacter infections and for scientific research on the properties of pathogenicity, virulence and infectivity of Helicobacter, as well as host defense mechanisms. The present sequence is Helicobacter sp. HP30-derived peptide
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HP30; HP56; immune response; therapy; Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                              HP30, HP56; immune response; therapy, Helicobacter infection; vaccine; type B gastritis; antiinflammatory; adenocarcinoma; defense mechanism; low grade B cell lymphoma; virulence; antibacterial; gastric cancer; immunostimulant; cytostatic; peptic ulcer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breast cancer-associated protein fragment BC-2 SEQ ID NO:12
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Matches:
Conservative:
Mismatches:
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 Helicobacter sp. HP30-derived peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 115; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW44365 standard; peptide; 173
                                                                                                                                                                                                                                                                                                             Jackson WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-732-091-3 (1-759) x AAE26872
                                                                                                                                                                                                               07-DEC-2001; 2001WO-US048392.
                                                                                                                                                                                                                                            07-DEC-2000; 2000US-00732091.
                                                                                                                                                                                                                                                                             (ANTE-) ANTEX BIOLOGICS INC
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100.00%
100.00%
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                                                                                                                                                                                                                                                                                                             Tian J, Walker R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD44525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30 AA;
                                                                                                                                               W0200251237-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                               04-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW44365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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The present sequence represents a breast cancer-associated protein fragment for use in a method for diagnosing breast cancer in tissue or body fluid by detecting one or more breast cancer-associated protein(s). Alternatively a nucleic acid encoding a breast cancer-associated protein is detected in the sample by the use of a nucleic acid probe. The breast cancer-associated protein useful in diagnostic assays and kits for breast cancer detection. The proteins are also useful in screening for inhibitory compounds and monitoring effectiveness of treatments. The antibody, or pharmaceutical compositions containing the antibody or the inhibitory compound, can be administered to patients to treat breast cancer. The methods allow reliable and early diagnosis of breast cancer, or prediction of its but not in non-cancerous breast cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 TIGGIAAAGACGGCGAAAAAGACACAAIGAAAAACIGACCACCACCICCAIAGAAIACAAAA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GAAGGAGTCTTAI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing breast cancer by detecting a breast cancer-associated protein - allows early and reliable diagnosis and treatment monitoring, and antibody or inhibitory compounds useful for treating breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GlnLyeThrTrpValAlaProGlyTyrValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 GGCATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 ysserAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ACAAAGAGAITITIAIGCGAIGIGCGAIAAAITAAAGGICAAITACAACAAGAAAACIG
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 32; 47pp; English
                                                                                                                                                      97WO-US009529.
                                                                                                                                                                                                       96US-00658639
                                                                                                                                                                                                                                                                                                              Wu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101.50
43.58%
22.91%
7.52%
                                                                                                                                                                                                                                                          (MATR-) MATRITECH INC
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N-PSDB; AAV15304.
                                                                                                                                                                                                                                                                                                            Keesee SK, Obar R,
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Best Local Similarity:
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Homo sapiens
                                                 WO9746884-A1
                                                                                                                                                      03-JUN-1997;
                                                                                                                                                                                                       05-JUN-1996;
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0×2×6×6×8×2

Length: Matches: Conservative: Mismatches: Indels:

0.0325 101.50 43.58% 22.91% 7.52%

Percent Similarity: Best Local Similarity:

Query Match:

Sequence 173 AA;

Alignment Scores: Pred. No.:

Score:

Gaps

US-09-732-091-3 (1-759) x AAB98717 (1-173)

δλ	26	TGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGATTTGTTTG	82
qa	2	  TrpProSerLysAlaArgTrpMetLeuPheAlaSerTrp	14
ζ	98	TIGGIAAAGACGGCGAAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAA	145
ДÜ	15		25
λō	146		205
තුර	26	LysPheValLeuMetArgalaAsnIleGlnAlaValSerLeuLysIleGlnThrLeuL	<b>77</b>
ò	206	GGAGCAATAGITITGCGAGITITCAITAAAGGCGAAGGAGTCTTAI	250
, ਰੂਨ	45	ysSerAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA	65
ò	251	ACAAAGAGATTTTATGCGATGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTG	310
q	65	snargglnLeuLysLeuProGlnIleGlnLysIleMetMetGluPheGluArgGlnAlaG	92
λδ	311	AAACGACTITAAITGAACAAAAATGCITICIAAAAICTIAGAAAGAAGITIGGAAGAAA	370
f f	85		105
ζŎ	371	TGGATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAA	415
qa	105		125
λõ	416	AAAACACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAA	475
qQ	125	erLeuThrAspGluLeuSerAsnLeuProSerThrGlyGlySerLeuSerValAlaA	144
Š	476		
qq	144	laglyGlyLysLysAlaGluAlaAlaAlaSerAlaLeuAl	
Search co Job time	omple : 69	Search completed: July 5, 2004, 03:03:13 Job time : 69 secs	

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

protein search, using frame\_plus\_n2p model OM nucleic - ; Search time 22.5 Seconds 5, 2004, 03:00:58 Run on:

{without alignments)
6489.722 Million cell updates/sec

US-09-732-091-3 Perfect score: Title:

1 atggcatacaaatatgatag.......... Sequence:

**BLOSUM62** Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

283366 segs, 96191526 residues

of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters: -MODEL=frame+\_n2p.model -

Database

1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		¥0				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	1279	94.8	1	2	D64718	conserved hypothet
2	1270	94.1		N	B71800	hypothetical prote
м	784.5	58.2		N	E64718	conserved hypothet
4	630	46.7		N	A71800	hypothetical prote
'n	472.5	35.0	155	N	C64718	conserved hypothet
9	265	19.6		N	C64721	hypothetical prote
7	265	19.6		~	AC0503	conserved hypothet
ω	262	19.4		N	C30630	probable oxidoredu
σ	262	19.4		Ċ	C85481	probable oxidoredu
10	133	9,6		N	F64718	hypothetical prote
c 11	127.5	9,5		۲۷	D90630	hypothetical prote
c 12	127.5	9.5		~1	D85481	hypothetical prote
c 13	122	9.1		N	A40623	heat shock protein

hypothetical prote conserved hypothet probable D-2-hydro probable ATP (GTP	hypothetical prote probable preprotei 8-amino-7-oxonoman hymothetical prote	Applications proceed probable permease abortive phage res hypotherical prote bullous pemphicoid bullous pemphicoid	hypothetical prote penicillin amidase transposase ISC122 exodeoxyribonuclea	hypothetical prote penicillin amidase hypothetical prote hypothetical prote repeat organellar RNA polymerase siq	molog cal pr otein membra	body-wall muscle t hypothetical prote hypothetical prote transposase-like p
AE0360 G90546 C81380 A81385	A70144 E71330 G70355	133071 F96920 A47025 C81327 A40937	A86302 S49252 E90488 G70178	T33070 I39665 T16536 H81345 T18372	A64320 T24622 S42797 S53378 E64477	A45488 AI2368 B97214 E64571
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282 1099 311 728	346 916 373	3 4 2 0 2 4 4 2 0 4 4 2 0 4 4 4 2 0 4 4 4 2 0 4 4 4 9 4 9 4 9 9 9 9 9 9 9 9 9 9 9 9	387 802 355 610	430 802 308 1939	508 508 615 1769	284 359 440
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conserved hypothetical protein HP1588 - Helicobacter pylori (strain 26695) (Species: Helicobacter pylori C;Species: 99-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999

C;Accession: D64718

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MuID:97394467; PMID:9252185
A;Accession: D64718
A;Accession: D64718
A;Accession: D64718
A;Residues: 1-253 < COM>
A;Residues: 1-253 < COM>
A;Coss-references: GB:AB000656; GB:AB000511; NID:92314771; PIDN:AAD08627.1; PID:92314

Length:
Matches:
Conservative:
Mismatches:
Indels: 1.5e-97 1279.00 100.00% 100.00% 94.81% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: Score:

US-09-732-091-3 (1-759) x D64718 (1-253)

Gaps:

9	0
1 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA 60	1 MetalaTyrLysTyrAspArgAspLeuGluPheLeuLysGlnLeuGluSerSerAspLeu 20

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21 LeuaspLeuPheGluValLeuValPheGlyLysAspGlyGluLysArgHisAsnGluLys 40 TIGGATITIGITIGAGGIGCTTGTTTTTGGTAAAGACGGCGAAAAAAGACACAATGAAAAA 녆 g ₽

121 CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 180

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C89910

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7.3

98.5

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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Aug-1997
C;Accession: E64718
C;Accession: E64718
Extromb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loffus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKelson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A,Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A,Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A,Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 180
                                                                                                                                                                                                                                                      GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-207 <TOM> A;Residues: 1-207 <TOM> A;Cross-references: GB:AE000511; TIGR:HP1589 C;Genetics:
                                                                                                                                                                                                                                                                                                                                   161 GlypheLysSerTyrGlnLeuAlaVall1EvalAlaAsnAlaValAlaLysThr11eLeu
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                           21 LeuAspLeuPheGluValLeuValPheGlyLysAspGlyGluLysArgHisAsnGluLys
                                                                                                                                                                                                             61 IlealaGluLeuGlnTyrTyrGlySerAsnSerPheAlaSerPheIleLysGlyGlu
                                                                                                                                                                                                                                                                    81 GlyValLeuTyrLysGluIleLeuCysAspValCysAspLysLeuTyrValRenTyrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGCGTGGTTTATCGCTTGCGGGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACA
                                                                                                                                                               41 LeuThrSerSerileGluTyrLysArgHisGlyAspAspTyrAlaLysTyrAlaGluArg
                                                                                                                                                                                             ATCGCTGAAGAGTTGCAATACTATGGCAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                                                                                                                                                                                                                                                                                   TIGGAAGAAATGGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAC
            atggcatacaaatatgatagagacttggaatttttaaagcaattggaatctagtgattta
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(E64718)
Conserved hypothetical protein HP1589 - Helicobacter pylori (strain 26695)
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B71800
C;Pgecies: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
A;Variety: strain 1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: B71800
C;Accession: B71800
C;Accession: B71800
C;Accession: B71800
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD: 99120557; PMID: 9923682
A;Accession: B71800
A;Accession: B71800
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A;Accession: B71800
A;Accession: B71800
A;Accession: B71800
A;Coss-references: GB.AE001571; GB.AE001439; NID: 94156120; PIDN: AAD07073.1; PID: 9415612
C;Genetics:
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                                             ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                                                                                                                                     TTGGAAGAAATGGATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAAC
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Conserved hypothetical protein HPIS87 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Accession: C64718
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: C64718
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Matches:
Conservative:
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hypothetical protein jhp1493 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
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C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 12-Feb-1999 #sequence_revision 02.7; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
I ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Title: Genomic A;1800
A;Accession: A;1800
A;Accession: A;1800
A;Accession: A;Bashanay
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A,Residues: 1-155 <tom> A,Cross-references: GB:AE000656; GB:AE000511; NID:g2314771; PIDN:AAD08626.1; PID:g231477</tom>	4.92e-14 Length: 265.00 Matches:
nt Scores: 3.99e-31 Length: 472.50 Matches:	Percent Similarity: 48.99\$ Conservative: 44 Best Local Similarity: 31.17\$ Mismatches: 90 Query Match: 19.64\$ Indels: 36 DB: 2 Gaps: 6
Percent Similarity: 78.23\$ Conservative: 22 Best Local Similarity: 63.27\$ Mismatches: 29 Conservation 15 C1\$ Index 1.29	US-09-732-091-3 (1-759) x C64721 (1-237)
	Oy 7 TACAAATAIGAIAGAACIIGGAAITIITIAAAGCAAIIGGAAICIAGIGAIITIAIIGGAI 66
US-09-732-091-3 (1-759) x C64718 (1-155)	Db 5 TyrLeuAsnAspSerAspIeuAspPheLeuGlnHisCysSerGluGluGlnLeuAlaAsn 24
Oy 112 AATGAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATAC 171	Qy 67 TIGITIGAGGIGCITGITTITGGIAAAGACGGCGAAAAAAAGACACAATGAAAAAACIGACC 126
Oy 172 GCAGAAAGAATCGCTGAAGATTGCAATACTATGGGAGCAATATTTGCGAGTTTCATT 231	Oy 127 AGCTCCATAGAATACAAAGGCATGGCGATGATTACGCTAAATACGCAGAA 177 ::: ::: ::: ::: ::: :::       ::: :::
OY 232 AAAGCGAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTC 291 :::	OY 178 AGAATCGCTGAAGAGTTGCAATACTATGGGGGATAGTTTTGCGGAGTTTCATTAAGGC 237
Qy 292 AATTACAACAAGAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATCTTA 351	Oy 238 GAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGCGATAAATTAAAGTCAATTAC 297
OY 352 GAAAGAAGTITIGGAAGAAATGGAIGAIGAAGAAAGAAAATGIGCGAIGAATTAICC 411 :::	OY 298 AACAAGAAAACGACTTTAATTGAACAAAAACHGCTTTCTAAAATCTTAGAAGA 357 :::   :::
OY 412 ATABABARCAGGACABITTAAACAGACAAGCCTTAAGCGCGCGACTTTA 462 :::	Oy 358 ACTTTGGAAGAAATGGATGATGAA
Oy 463 ACGCIGITIAAAATGGGGGGILITAAAATCTIAICAATTAGCIGICATTGTIGCGAAIGCG 522	OY 385 GTGAAAGAAATGGGGTGAAATTATCCATAAAAAACACGGACAATTTAAACAGACAAGCC 444
Oy 523 GTCGCAAAAACCATTCTAGGG 543 ::: :::         Db 142 MetValArgGlnThrLeuGly 148	Qy 445 TTAAGCGCGGCGACTTTAACGCTGTTTAAATGGGGGTTTTAAATCTTATCAATTAGCT 504
	Oy 505 GTCATTGTTGCGAATGCGGTGCTTTTTTGGTGTGCTTTGTTGCTTGC

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A,Title: Complete genome sequence of a multiple drug resistant Salmonella enter A,Reference number: ABC502; MUD:21534947; PMID:11677608
A,Accession: AGO503; MUD:21534947; PMID:11677608
A,Status: preliminary
A,Status: preliminary
A,Recidues: 1-237 < PAR>
A,Recidues: 1-237 < PAR>
A,Cross-references: GB:AL513382; PIDN:CAD01163.1; PID:g16501293; GSPDB:GN00176
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probable oxidoreductase ECSD012 [imported] - Escherichia coli (strain 0157:H7, substicispecies: Bscherichia coli
C;Species: Bscherichia coli
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C;Accesion: C90630
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, (gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res 8, 11-22, 2001
A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Accession: C90630
A;Accession: C90630
A;Molecule type: DNA
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A;Residues: 1-237 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33434.1; PID:g13359467; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS0012
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AsplysGluMetSerThrPheGluIleGluGInGInLeuLeuGluGlnPheLeuArgAsn 124
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| ArgileLeuArgThrHisAlaAlaMetSerValLeuGlyHisGlyLeu---LeuArgGly
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165 ValSer----
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	A,Molecule type: DNA A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom> A,Residues: 1-39 <tom 1-39="" 1-39<="" <tom="" a,residues:="" th=""><th>QY         1 ATGGCATACAAATATGATAGAATTTTTAAAGCAATTGGAATTTTAAAGCAATTTGGAATTTTA         60           Db         1 MetalaTyraxgTyraspSerAspLeuGluDheLeuLysArgLeuSerSerSerSerAspLeu         20           Qy         61 TTGGATTTGTTTGAGTGCTTGTTTTTGGTAAAAAAGACGCGAAAAAAAGACACAATGAA         117           Db         21 LysAspLeuPheAspAlaLeuValTyrAspGluAspGlvThrLeuArgMetAsnGlu         39</th><th>RESULT 11 1990630 hypothetical protein ECs0011 [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: D90630 R; Hartori, M.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001 A; Tatle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gasawara; Reference number: A99629; WUID:21156231; PMID:11258796 A; Steference number: A99629; WUID:21156231; PMID:11258796 A; Status: preliminary A; Molecule type: DNA A; Status: Calliminary A; Molecule type: DNA A; Cross-references: GB:RA000007; PIDN:BAS33435.1; PID:g13359468; GSPDB:GN00154 A; Experimental source: strain O157:H7, substrain RIMD 0509952 C; Genetics: A; Genetics</th></tom></tom></tom></tom></tom></tom></tom></tom>	QY         1 ATGGCATACAAATATGATAGAATTTTTAAAGCAATTGGAATTTTAAAGCAATTTGGAATTTTA         60           Db         1 MetalaTyraxgTyraspSerAspLeuGluDheLeuLysArgLeuSerSerSerSerAspLeu         20           Qy         61 TTGGATTTGTTTGAGTGCTTGTTTTTGGTAAAAAAGACGCGAAAAAAAGACACAATGAA         117           Db         21 LysAspLeuPheAspAlaLeuValTyrAspGluAspGlvThrLeuArgMetAsnGlu         39	RESULT 11 1990630 hypothetical protein ECs0011 [imported] - Escherichia coli (strain O157:H7, substrain C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C; Accession: D90630 R; Hartori, M.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001 A; Tatle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gasawara; Reference number: A99629; WUID:21156231; PMID:11258796 A; Steference number: A99629; WUID:21156231; PMID:11258796 A; Status: preliminary A; Molecule type: DNA A; Status: Calliminary A; Molecule type: DNA A; Cross-references: GB:RA000007; PIDN:BAS33435.1; PID:g13359468; GSPDB:GN00154 A; Experimental source: strain O157:H7, substrain RIMD 0509952 C; Genetics: A; Genetics
GACAGCGATTGATATTGCAGGSCCGGCTTATAGGSTAACCATACCGGCATGC 684 sala	City: 30.77%  19.42%  2  L-759) x C85481 (1-237  AAATATGAAAGAGACTTGGAAA GenAsnAspSerAspLeuAspE  ITTGAGGTGCTTGTTTTGGTR  TTTGAGGTGCTTTTTTGGTR  A 3 2 2 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2	127 127 45 178 65	

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A;Residues: 1-206 <STO>
A;Cross-references: GB:AE005174; NID:g12512690; PIDN:AAG54312.1; GSPDB:GN00145; UMGP:3
A;Experimental source: strain 0157:H7, substrain EDL933
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heat shock protein htgA - Escherichia coli (strain K-12)
N.Alternate names: heat shock protein Y
C.Species: Escherichia coli
C.Species: 21-Sep-1993 #sedeunce revision 18-Nov-1994 #text_change %1-Mar-2002
C.Accession: A40623; A56688; D64721; S28460
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C;Superfamily: Escherichia coli heat shock protein htgA
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R;Missiakas, D.; Georgopoulos, C.; Raina, S.  J. Bacteriol. 175, 2613-2624, 1993  J. Hacteriol. 175, 2613-2624, 1993  J. Hacteriol. 175, 2613-2624, 1993  J. Reference number: A40623, MUID:93239687; PMID:8478327  A;Reference number: A40623, MUID:93239687; PMID:8478327  A;Recession: A40623  A;Recission: A60623  A;Recission: A60623  A;Recission: Back of MID:950809  A;Reference number: A56688, MID:94003405; PMID:8400364  A;Reference number: A56688, MID:94003405; PMID:8400364  A;Recission: A56688  A;Recission: A56688  A;Recission: A56688  A;Recission: A56688  A;Recission: Back of MID:94003405; PMID:CAA47932.1; PID:941757  A;Roseute: Pre-Ferences: EMBL: K67700; NID:941754; PIDN:CAA47932.1; PID:941757  R;Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A.; Rose, D.J.; Mau, B.; Shao, Y.  Science 277, 1453-1462, 1997  A;Reference number: A64720; MUID:97426617; PMID:9278503  A;Reference number: A64720; MUID:97426617; PMID:978803  A;Reference number: A64720; MUID:97426617; PMID:978803  A;Reference number: A64720; Muid: Shown; translation not shown	2; GB:U00096; NID:g1786192; F K-12, substrain MG1655 r Met-1 (CTG) or Met-36 is th i heat shock protein htgA i heat protein Length: 196 Matches: 51	Dercent Similarity: 38.41\$   Conservative: 12     Description   1.10\$   Mismatches: 65     Description   2.05\$   Indels: 36     Description   2.05\$   Gaps: 5     US-09-732-091-3 (1-759)   X 440623 (1-196)     Qy	17	Oy 398 CACATTCTTTCACT

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31 LeuLeuAspLysGluLeuSerAspLeuArgAsnGlnAspGluGluMetThrArgGluArg 110
                                                                                                                                                                 167 LeuLeulleLeuHisGlyAlaAsnAsnIleValGluSerGlyTyrTleLeuTyrArg 186
        286 AAGGTCAATTACAACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAA 345
                                                                                                                                          GTGAAAGAA---ATGTGCGATGAATTATCCATAAAAAACACGGACAATTTAAACAGACAA 441
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                                          SerSerAspIleThrAlaLysValAsnThrGlyGlufleThrThrGluThrAlaIleLys
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AE0360
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I), M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A; Status: preliminary
A; Molecule type: DNA
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A; Molecule type: DNA
CX cross-references: GB: ALS90842; PIDN: CAC92208.1; FID: G15980920; GSPDB: GN00175
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	107	Q9zj24 helicobacte	O26106 helicobacte	Q9zj25 helicobacte	P75617 escherichia	P58316 escherichia	P28697 escherichia	Q90474 brachydanio	O83394 treponema p	O66875 aquifex aeo	Q01457 lactococcus	Q9pn86 campylobact		042184 gallus gall	Q60136 bacillus me	P31956 arthrobacte	P46064 caenorhabdi	P77994 thermatoga
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253 AA. PRT; STANDARD;

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ALIGNMENTS

16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein HP1588. 026107.1 16-0CT-2001 (Rel. 40, Created) HP1588

Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter. NCBI\_TaxID=210;

STRAIN=26655 / ATCC 700392;
STRAIN=26655 / ATCC 700392;
STRAIN=26655 / ATCC 700392;
STRAIN=26655 / ATCC 700392;
Toch U.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Toch U.-F., White D., Kechum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush U., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Dergo D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

The complete genome sequence of the gastric pathogen Helicobacter Venter J

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Nature 388:539-547(1997).
-!- SIMILARITY: Belongs to the UPF0174 family. DER PROPERTIES DE LA PORTIES DE LA PROPE

EMBL; AE000656; AAD08627.1; -. PIR; D64718; D64718.

G.F.

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                                                                                                                                                                                                       "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the UPF0174 family.
                                       Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                  MEDLINE=99120557; PubMed=9923682; King B.L., Brown E.D., Doig P Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Carmel G., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis Crust T.J.;
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PIR; B71800; B71800;
Interpro; IPR005367; UPF0174.
Pfam; PF05657; UPF0174; 1.
Hypothetical protein; Complete proteome.
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 InterPro; IPR005367; UPF0174.
Pfam, PF03667; UPF0174, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 253 AA; 28417 MW; 00E15A38B1A2036A CRC64;
                                                                                  GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT 759
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Matches:
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ID YF88 HELPJ
AC Q9ZJZ4;
DT 16-OCT-2001
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               GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
                                                                                                         GGGCGTGGTTTATCGCTTGCGGCCAATCAGGTGCTTACAAGAACTCTGAGCTTTTAACA
                                                                                                                       GGTCCTGTTGGCTGGATCATTACAGGCGTATGGACAGCGATTGATATTGCAGGGCCGGCT
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STRAIN=26695 / ATCC 700392;

STRAIN=27394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Relson K., Qackerbusk J., Zhou L., Kirkness B.F., Peterson S.,

Nocktus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Jtterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin B.,

Hayes W.S., Borodovsky M., Kaip P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished observations (OCT-2001).
-!- SIMILARITY: Belongs to the UPF0174 family.
-!- CAUTION: Ref.1 sequence differs from that shown due to frameshift in position 160.
                                                                                                                                                                                                                                                                          GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT 759
                                                                                                                                                                                                                                                                                          AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal 253
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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Relicobacter pylori (Campylobacter pylori)
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Helicobacteraceae, Helicobacter.
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Nature 388:539-547(1997)
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16-0CT-2001
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AATTACAACAAGAAAACGAACTTTAATTGAACAAAACATGCTTTCTAAAATCTTA 351
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LysAspSerLeuGluIysMetSerArgArgGluIleLysGluLeuCysAsmGluLeuGly 101
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
      proteome.
F98D3FB8F3F62323 CRC64;
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                                                                                                                                                                                                                                                                                                                                 US-09-732-091-3 (1-759) x YF87_HELPY
1 protein; Complete
209 AA; 23069 MW;
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(Rel. 40, Last seq
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47.22%
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Best Local Similarity:
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Hypothetical
SEQUENCE 20
                                                                                           Alignment Scores:
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182 IleAsnLeuAlaGiyProAlaTyrArgValThrValProAlaCysValLeuValAlaThr 201
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5 TyrLeuAsnAspSerAspLeuAspPheLeuGlnHisCysSerGluGluGluLeuAlaAsn
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
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-!- SIMILARITY: Belongs to the UPF0174 family.
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MEDLINE=94003405; PubMed=8400344;
James R., Dean D.O., Debbage J.;
Five open reading frames upstream of the dnak gene on the Seq. 3:327-332(1993).
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Matches:
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Enterobacteríaceae; Escherichia.
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          Doig P.C.,
                                                                                                                                                                            two unrelated isolates of the human
       Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C. Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Xills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.)
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C6EC950CDD424CAF CRC64;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                        "Genomic sequence comparison of two unrelated :gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Camplete SEQUENCE 209 A4; 22907 MW;
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630.00
75.49%
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|HisGlyLysLeuTyrArgAlalleLeuLeuAspValSerLysArgLeuLysAla 104
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                                                                                                                                                                                         GTGAAAGAAATGTGCGATGAATTATCCATAAAAACACGGACAATTTAAACAGAAAGCC 444
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                   ArgasnGluLeuPheLysSerMetGluGlyHisProGluGlnHisArgArgAsnTrpGln
                                                                          leulleAlaGlyGluLeuGlnHisPheGlyGlyAspSerIleAlaAsnLysLeuArgGly
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                                                        178 AGAATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGC
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STRAIN=0157.H7 / BDL933 / ATCC 700927;

MEDLINE=1074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., MayNew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., MayNew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., MayNew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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LeuGlnIleAlaCysLeuArg 229
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STRAIN=C157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
127 AGCTCCATAGAATACAAAAGG---
                                                                                                                                                                                                                                  AGTTTGGAAGAAATGGATGATGAA
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YAAW OR ZOULI OR ECSO012.
Escherichia coli 0157:H7.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its see by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohfeubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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ArgasnGluLeuPheLysSerMetGluGlyHisProGluGlnHisArgArgAsnTrpGln
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145 ValAsnGluLeuGluGluLeuLeuProLeuMetLysAspLysLeuLeuAlaLysGly
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                                                                      comparison with a laboratory strain K-12."; 01).
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Mismatches:
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Matches:
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Pfam; PF03667; UPF0174; 1.
Hypothetical protein; Complete SBQUENCE 237 AA; 26681 MW;
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8:11-22(2001).
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PIR; C90630; C90630.
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EMBL; X67700; CAA47932.1; ALT INIT.
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   be deleted in future releases.
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Hypothetical protein; Heat shock.
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(Rel. 40, I
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ID HS9A_BRARE
AC Q90474;
DT 15-JUL-1999
DT 15-JUL-1999
DT 16-OCT-2001
                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                          205
                                              624
                                                                                                       684
                                                                                                                        "THE COMPLETE GENOME SEQUENCE OF ESCHETICHIA COLI K-12.";
Science 277:1453-1474(1997).

-! FUNCTION: NOT KNOWN, REQUIRED FOR HIGH-TEMPERATURE GROWTH OF

E. COLI. IT IS POSSIBLE THAT HYPA PROTEIN SOMEHOW REGULATES BITHER

TRANSCRIPTION OF THE RPOH GENE OR THE ACTIVITY OF ITS GENE PRODUCT

SIGMA-32. PLAYS A ROLE OPPOSITE THAT OF DMAK, DMAJ, AND GRPE IN

TERMS OF HEAT SHOCK REGULATION, ANTAGONIZING THE NEGATIVE OF

THESS AND THUS FINE-TUNING THE HEAT SHOCK RESPONSE.

-! INDUCTION: By high Lemperatures.

-! CAUTION: It is uncertain whether Met-l or Met-36 is the initiator.

-! CAUTION: Ref.3 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frameshift.
CAUTION: This sequence, according to the EcoSeq database (K. Rudd) is probably not a real protein; therefore this entry will probably
                                            AATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACAGGTCCTGTTGGCTGGATCATTACA
                                                                          --AlaGlyteuGlyélyérovalólyAlaAlaLeuAsn
                                                                                                     GGCGTATGGACAGCGATTGATATTGCAGGGCCGGCTTATAGGGGTAACCATACCGGCATGC
                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Very hypochetical heat shock protein htgA (Heat shock protein htpY)
HTGA OR HTPY OR B0012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503; Blach C.A., Perna N.T., Burland V Blattner F.R., Plunkett G. III, Blach C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yura I., Mori H., Nagai H., Nagata I., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; "Systematic sequencing of the Escherichia coli genome: analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A..
SEQUENCE FROM N.A..
SEQUENCE FRAINERLS / Wallo,
STRAINERLS / Wallo,
MEDLINES 23.96871, PubMed=8478327;
A. Missiakas D., Georgopoulos C., Raina S.;
A. Missiakas D., Georgopoulos C., Raina S.;
RT "The Escherichia coli heat shock gene htpy: mutational ana. RT cloning, sequencing, and transcriptional regulation.";
RT cloning, Sequencing, and transcriptional regulation.";
RT Cloning, Sequencing, and transcriptional regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             James R., Dean D.O., Debbage J.;
"Five oper reading frames upstream of the dnaK gene of
                                                                                                                                                                                                                                                     196 AA
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Nucleic Acids Res. 20:3305-3308(1992)
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                 685 ATTGTGGTTGCCACTTTACGC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12;
MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94003405; Pubmed=8400364;
                                                                                                                                                                                                                                                     STANDARD:
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STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629 ACGCCTGTAATGATCCAGCCAACAGGACCTGTTAAAAAGCTCAGAGTTCTTGTAAGCACC 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 ACAAIGACAGCTAATTGATAAGATTTAAAA-----CCCCCCGTTTTAAACAGCGTTAAA 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LysMetArgValSerTrpLeuGluSerLysCysAspThrProPheAlaAsnAsn----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 ATTICITICGAACTICITICIAAGATITITAGAAAGCAIGITITIGITICAATTAAAGICGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 AA; 21225 MW; ECA6154160A40993 CRC64;
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Last sequence update)
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661 TATAGGGTAACCATACCGGCATGCATTGTGGTTGCCACTTTACGCCTAAAAACACGCAA 720
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                                                            247 TTATACAAA----GAGATTTTATGCGATGTGGCGATAAATTAAAGGTCAATTACAACAAG 303
                                                                                                                                              364 GAAGAAATGGATGAAGAAGAGTGAAAGAAATGTGCGATGAATTATCCATAAAAACACG 423
                                                                                                                                                                                                                                                                                                                 GACAATTTAAACAGACAAGCCCTTAAGCGCGCGACTTTAACGCTGTTTAAAATGGGGGGT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spirochete.",
Science 281:375-388(1998).
-!-FUNCTION: Involved in protein export. Interacts with the secY/secE
-!-FUNDUICN: SecA has a central role in coupling the hydrolysis of
ATP to the transfer of pre-secretory periplasmic and outer
membrane proteins across the membrane (By similarity).
                                                                                                 513 IleTyrMet11eGluPro11eAspGluTyrCysValGlnGlnLeuLysGluTyrAspGly
                                                                                                                                                                                                                                                                        544 GinLeuProGluAspGluGluGluLysLysLysGlnAspGluLeuLysAlaLys---Tyr
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| LysAspGlnValAlaAsnSerAlaPheValGluArgLeuArgLysAlaGlyLeuGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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STRAIN-Nichols;
MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
28-FEB-2003 (Rel. 41, Last ann
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GluAsnLeuCysLys-
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LeuSerAspLeuLeuArgTyrTyrThrSerAlaSerGlyAspGluMetValSerLeuLys 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --TTCATTAAAGGCGAA---
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                               zebrafish and
                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the heat shock protein 90 family.
                                                                                                                                                                                                                                                                                                                                                                             (<u>B</u>
                                                                                                                                                                                     Lele Z., Hadfi S., Sass J.B., Krone P.H.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           MEDLINE=95071389; PubMed=7980538; Krone P.H., Sass J.B.; Krone P.H., Sass J.B.; Krone P.H., Sass J.B.; Else and HSP 90 beta genes are present in the sare differentially regulated in developing embryos."; Biochem. Biophys. Res. Commun. 204:746-752(1994).
-!- FUNCTION: Molecular chaperone. Has ATPase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F7DEB8EF1FBC9CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    726
61
41
75
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                  Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P07900; 1BYQ.
ZZIN; ZDB-GENE-990415-94; hsp90a.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
Pfam; PPC2518; HATPase c; 1.
Pfam; PF00183; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Heat shock 726 AA; 83561 MW; F7DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-732-091-3 (1-759) x HS9A_BRARE
protein HSP 90-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF068773; AAC21567.1; -.
EMBL; L35586; AAA97518.1; -.
PIR; JC2343; JC2343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00775; HEATSHOCK90.
SWART; SM00387; HATPASE C; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.537
105.00
35.79%
21.40%
7.78%
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                       NCBI_TaxID=7955;
  Heat shock protests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415
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                                                                                                  ---AlaLeuLeuArgThrArgGlyValLyBHisGluValLeu 486
                                                                                                                                                                                      487 AsnAlaLysAsnHisAlaArgGluAlaLeuileileAlaGluAlaGlyAlaLysGlySer 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392:353-358(1998).

-!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-aminc-7-oxonoananaet + CoA + CO(2).

-!- COFACTOR: Pyridoxal phosphate (By similarity).

-!- COFACTOR: Pyridoxal phosphate; first step.

-!- PATHWAY: Biotin biosynthesis; first step.

-!- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                 :::||| :::||| 525
507 ValThrileAlaThrAsnMetAlaGlyArgGlyThrAsplleLysLeuGlyGlyAsn
456 GlyGlnProValleuValGlyThrIleSerIleGluLysSerGluLysLeuSer-----
                                                                                                                                                                                                                                                                                                                                                                                                       30-MXY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxononanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7-ketopelargonate synthase) (7-keto-8-amino-pelargonic acid synthetase)
(7-KAP synthetase) (L-alanine--pimelyl CoA ligase).
                                                               442 GCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGTTTTAAATCTTATCAATTA
                                                                                                                                                                                                                                    ----TIATCGCTTGCGGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber J.
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                   ---GCTGTCATTGTTGCGAATGCG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536B34A5D5F84401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotin biosynthesis; Transferage; Pyridoxal phosphate;
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Matches:
                                                                                                                                                                                                                                      -----GICGCAAAACCATTCTAGGGCGTGGT-
                                                                                                                                                                                                                                                                                                                                                               373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P12998; 1BSO.
InterPro; IPR003408; Ala synthase.
InterPro; IPR004839; Aminotrans_I/II.
InterPro; IPR001917; Aminotrans_II.
InterPro; IPR004723; BioF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02490; ALA Bynchase; 1.
Pfam; PF00155; aminotran 1 2; 1.
TIGREAMS; TIGR00858; bioF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000699; AAC06836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00599; AA TRANSFER
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96.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
BINDING 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOF OR AQ 626.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                   BIOF AQUAE
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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LeuSerGluGluGluJysTrpSerAlaIleCysAspGluIleLysGluAlaHisThrArg 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 PheLysTyr------IleHisTyrPheThrGlnAlaLeuArgAlaHisLeuLeuTyr 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 ArgalaaspvalaspTyrValValLysaspGlyGlnValGlnIleValAspGluPheThr 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------AAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAA 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 GlyMetThrGlyThrAlaAspThrGluAlaLeuGluLeuAsnLysIleTyrLysLeuGlu 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGACTITAATIGAACAAACAIG---CITICIAAAAICITAGAAAGAAGTITGGAAGAA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TIATCCATAAAAACACGGACAATTTAAACAGACAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AGGCATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 GGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATT---
        SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secA, secB, secD, secE, secF, secG and secY (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PROU906; SECĀ.
TIGRFRMs; TICRO0965; secA; 1.
PROSTTE; PSO1312; SECA; 1.
Protein transport; ATP-binding; Membrane; Translocation; Transport;
                                                         similarity).
SUBCELLULAR LOCATION: Cytoplasmic side of plasma membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EASS61F6EE7C65AE CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   916
52
44
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76
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL)

    -! SIMILARITY: Belongs to the secA family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                   entities requires a license agreement (St or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                             PIR; E71330; E71330.
TIGR; TP0379; -
InterPro; IPR004027; SEC C_motif.
InterPro; IPR004085; SecA.
Pfam; PF02810; SEC-C; 1.
Pfam; PF01043; SecA_protein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-732-091-3 (1-759) x SECA_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103779 MW;
                                                                                                                                                                                                                                                                                                                        EMBL; AE001217; AAC65365.1; -.
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40.17%
21.76%
7.19%
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MP BIND 103
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                                                                                            similarity)
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DB:
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                                                                                                                                                                                                                                                                                                                                                 119 AlaSerIleIleAspGlyValArgLeuSerLysAlaGlnLysArgValPheLysHisLys 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 AspLeutysArgLeuThrGlnIleCysGluGluTyrAspCysMetLeuTyrIleAspGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGGTAAAGACGGGGAAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAA 144
                                                                                                                                                                                                                                            -----GAAGGAGTCTTATAC 252
                                                                                                                                                                                                                                                                                    253 AAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTGAA 312
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                                                                                                                                                                         52 LysGluAlaGlyLeuGlySerGlyAlaSerGlnLeuValSerGlyTyrThrLysHisHis 71
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                                                                        TIGGAAITITIAAAGCAAITGGAAICTAGIGAITTAITGGAITITGTITGAGGIGCTIGIT 84
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                                                                                                                                     -GlyLeuArgLysHisProGluValValGluGluSerileArgValLeu
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                                                                                            plasmid pIN20.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                   phage resistance
                                                                                                                                                                                                                                                                    Durmaz E., Higgins D.L., Klaenhammer T.R.;
"Molecular characterization of a second abortive phage resistangene present in Lactococcus lactis subsp. lactis ME2.";
G. Bacteriol. 174:7463-7469(1992)
-!- FUNCTION: PROVIDES RESISTANCE TO BACTERIOPHAGE BY ABORTIVE
                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA6E41E71B4A003C CRC64;
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01-OCT-1993 (Rel. 27, Last annotation update)
Abortive phage resistance protein abiC.
BEC OR PRF.
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OY 427 AATTTBAACAGACATAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGTTTT 486 Db 238 GlylleLeuArgThrGlnLeuSer245	OY 487 AAAICTIATCAATTAGCTGATGTTGTTGCGAATGCGGTCGCAAAAACCATTCTAGGG 543	Qy 544 CGTGGTTTATCGCTTGCGGCAATCAGGTG 573  Db 265 LeuGlylleGluLeulleGlyThrAsnLeu 274	15 6.	AC Q9PN86; DT 16-0CT-2001 (Rel. 40, Created) DT 16-0CT-2001 (Rel. 40, Last sequence update) DT 10-0CT-2003 (Rel. 42, Last armotation update)		OC Campylobacteraceae; Campylobacter.  NA NCBLTAXID=197; RN [1] RP SEQUENCE_FROM N.A.		Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.; "The genome secuence of the food-borne pathogen Campylobacter i	ials hypervariable sequences."; state 403:655-668 (2000). SIMILARITY: Belongs to the UPF0144 family. SIMILARITY: Contains 1 HD domain.	-!- SIMILARITY: Contains 1 KH domain. This SWISS-PROT entry is copyright. It is produced through a collaborat between the Swiss Institute of Bioinformatics and the EMBL outstatic			DR InterPro; IPR004087; KH dom. DR InterPro; IPR004087; KH dom. DR InterPro; IPR003607; Met_phsphohydro.			Alignment Scores: 3.41 Length: 517  Pred. No.: 95.00 Marches: 54 Score: Scoret Similarity: 38.04* Conservative: 43 Best Local Similarity: 21.18* Mismatches: 98 Query Match: 7.04* Indels: 60

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Stanley J.R., Tanaka T., Mueller S., Klaus-Kovtun V., Roop D., "Isolation of complementary DNA for bullous pemphigoid antigen by use of patients' autoantibodies."; J. Clin. Invest. 82:1864-1870/1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparison of molecularly cloned bullous pemphigoid antigen to desmoplakin I confirms that they define a new family of cell adhesion
                                                                                                                                 MEDLINE=93346806; PubMed=8345227;

Elgart G.W., Stanley J.R.;

"Cloning of the 5' mRNA for the 230-KD bullous pemphigoid antigen by amplification of LDNA ends.";
J. Invest. Dermatol. 101:244-246(1993).
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MEDLINE=96199235; PubMed=8621649;
Tang H.-Y., Chaffotte A.-F., Thacher S.M.;
"Structural analysis of the predicted coiled-coil rod domain of the cytoplasmic bullous pemphigoid antigen (8PAG1). Empirical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94280413; PubMed=8010969;
Hopkinson S.B., Jones J.C.;
"Identification of a second protein product of the gene encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2160-2767 FROM N.A.
MEDIINE=91216368; PubMed=2090522;
Owaribe K., Kartenbeck J., Stumpp S., Magin T.M., Krieg T.,
Diaz I.A., Franke W.W.;
"The hemidesmoscral plaque. I. Characterization of a major
constituent protein as a differentiation marker for certain forms
            TISSUE=Keratinocytes;
MEDLINE=22011493; PubMed=1717441;
Sawamura D., Li K., Chu M.-L., Uitto J.;
Sawamura D. pemphigoid antigen (BPAG). Amino acid sequences
"Human bullous pemphigoid antigen (BPAG). Amino acid sequences
deduced from cloned onNas predict biologically important peptide
segments and protein domains.";
                                                                                                                                                                                                                    TISSUE=Fetal brain, and Retina;
MEDLINE=96121334; PubMed=8575775;
Brown A., Dalpe G., Mathieu M., Kothary R.;
"Cloning and characterization of the neural isoforms of human
                                                                                                                                                                                                                                                                                                                          Laird G.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 Geerts D., Sonnenberg A.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB=Keratinocytes;
MBDL/IRS=91286285; PubMed=1712022;
Tanaka T., Parry D.A.D., Klaus-Kovtun V., Steinert P.M. Stanley J.K.
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 321-3214 FROM N.A. (ISOFORMS 1 AND 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unction plaque proteins.";
[, Biol. Chem. 266:12555-12559(1991)
                                                                                   Biol. Chem. 266:17784-17790(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epithelia."; Differentiation 45:207-220(1990).
  SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                           SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human epidermal autoantigen.";
Biochem. J. 300:851-857(1994).
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 392-492 FROM N.A.
TISSUE=Pineal gland;
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                                                                                                                                                                                                                                                                                             J. Biol. Chem. 277:5682-6687(2002).
-!- FUNCTION: Cytoskeletal linker protein. Anchors keratin-containing intermediate filaments to the inner plaque of hemidesmosomes. The proteins may self-aggregate to form filaments or a two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
                                                                                                                                                                         Okumura M., Yamakawa H., Ohara O., Owaribe K., *Novel alternative splicings of BPAGI (bullous pemphigoid antigen 1) including the domain structure closely related to MACF (microtubule
                                                                                    TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
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Note=No experimental confirmation available;
-:- TISSUE SPECIFICITY: Highly expressed in skeletal muscle and
globular domain-rod boundary.";
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IsoId=Q03001-2; Sequence=VSP_005053, VSP_005055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q03001-4; Sequence=VSP_005054, VSP_005056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q03001-6; Sequence=VSP_C05062,
Name=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isola=vo~v~.
Name=3; Synonyms=le;
Isold=Q03001-3; Sequence=VSP_05558,
VSP_05558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP 005064,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSP_005061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1;
IsoId=Q03001-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              me=6; Synonyms=EA;
IsoId=094833-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=7; Synonyms=EB;
IsoId=Q8WXK8-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=C94833-3; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homodimer.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U31850; AAC50243.1; -.
U31851; AAC50244.1; -.
AL096710; -; NOT ANNOTHED CDS.
AY032900; AAK63130.1; -.
                                                                                                                       TISSUE-Keratinocytes;
MEDLINE=21839111; PubMed=11751855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M69225; -; NOT ANNOTATED_CDS
EMBL; L11690; AAA52288.1; -.
localization of the N-terminal glo
J. Biol. Chem. 271:9716-9722(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY032901; AAK63131.1; -.
                                                                                                                                                                                                                                                                    actin cross-linking factor).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M63618; AAA35606.1; -. X58677; CAA41528.1; -. M22942; AAA35538.1; -. U04850; AAA57184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cultured keratinocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q03001-5;
                                                                                       SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BMBL:
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us-09-732-091-3.n2p.rsp

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                                                                                                                            2212 LysCysLeuGluGluAspLeuAlaLysSerGlnAsnLeuValSerGluPheLysGlnLys 2231
                                                                                                                                                                                             |||||||::: :::|||
2232 CysAspGlnGlnAsnIleIleGlnAsnThrIysLysGluValArgAsnLeuAsnAla 2251
                                                                                                                                                                   ---- AAAAACACGACAATTTAAACAGA 438
                                      ---AATTACAACAAGAAAACTGAAACGACTTTAATTGAACAAAACATGCTTTCTAAAATC
                                                                                          GAAGAAGTGAAAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griparic L., Keller T.C. III; "Identification and expression of two novel CLIP-170/Restin isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed predominantly in muscle.";
Biochim. Biophys. Acta 1405:35-46(1998).
-!- FUNCTION: SERMS TO BE A INTERNEDIATE FILAMENT ASSOCIATED PROTEIT THAT LINKS EMDOCYTIC VESICLES TO MICROTUBULES (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE CYTOSKELETON (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98137792; PubMed-9469933;
Griparic L., Volosky J.M., Keller T.C. III;
"Cloning and expression of chicken CLIP-170 and restin isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=042184-2; Sequence=VSP_000761;
Name=3; Synonyms=CLIP-170(11);
Isold=042184-3; Sequence=VSP_000762, VSP_000763;
Name=4; Synonyms=CLIP-170(11+35);
                                                                                                                                                                                                                                                                                                                     RESULT 14

REST CHICK STANDARD; PRT; 1433 AA.

AC 042184; 04228; 057563; 057564;

DT 15-UUL-1998 (Rel. 36, Created)

DT 15-UUL-1998 (Rel. 36, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DE Restin (Cytoplasmic linker protein-170) (CLIP-170).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bvent=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 17-1139 FROM N.A. (ISOFORMS 3 AND 4)
                                                                                        -TTAGAAAGAAGTTTGGAAGAAATGGATGAT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoid=042184-4; Sequence=VSP 000764; SIMILARITY: Contains 2 CAP-Gly domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1;
IsoId=042184-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Pectoralis muscle;
MEDLINE=99002898; PubMed=9784600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF014012; AAC60344.1; -. EMBL; AF020764; AAC60345.1; -. EMBL; AF045650; AAC03547.1; -.
                                                                                                                                                                     TGCGATGAATTATCCATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 206:195-208(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Glu 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                 439 CAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=2;
                                                                                                                                                                                                                                                                                     2252
                    292
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2175 ArgCysGluhlaLeuLysIleGlnAlaAspGlyPheLysAspGlnLeuArgSerThrAsn 2194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .:::::::: ::::|||||| | | ||::: |||| :::|||| SerPheArgAspGluLysGluLeuGluArgLeuGlnIleCysGlnArgLysSerAspHis 2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeurysGiuGlnPheGluLysSerHisGluGlnLeuLeuGlnAsnIleLysAlaGluLys 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                          GO; GO:0005604; C:basement membrane; TAS.
GO; GO:0005737; C:cytoplasm; IEP.
GO; GO:0005730; F:structural constituent of cytoskeleton; IEP.
GO; GO:0007010; P:structural constituent of cytoskeleton; IAS.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.
GO; GO:0045104; P:intermediate filament cytoskeleton organiza. .; IEP.
InterPro; IPR001589; Actbind actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001452; SH3.
InterPro; IPR001612; SH3.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2135 GluMetLeuLysGlnLysValGluGluLeuThrArgGlnAsnAsnGluThrLysLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCATACAAATATGAGAGTTTGGAATTTTTAAAG-----CAATTGGAATCTAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 GCGAGTTTCATTAAAGGCGAAGGA-----GTCTTATACAAAGAGATTTTATGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GAGGTGCTTTTTTGGTAAAGACGGCGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2115 GluAsrAsnAspLysIleGlnArgLeuAsnGluGluLeuGluLysSerAsnGluCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 AAATACGCAGAAAGAATCGCTGAAGAGTTG-----CAATACTATGGGAGCAATAGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; Actin-binding; Coiled coil; Repeat; 5H3 domain;
Structural protein; Cytoskeleton; Cell adhesion; Calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLOBULAR 1.
CENTRAL FIBROUS ROD DOMAIN.
GLOBULAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3214
46
35
35
38
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIN-BINDING.
CH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CH 2.
SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-732-091-3 (1-759) x BPA1_HUMAN (1-3214)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                SMART; SM00033, CH; 2.
SMART; SM00150; SPEC; 2.
PROSITE; PS50002; SH3; FALSE_NEG.
PROSITE; PS500019; ACTININ 1; 1.
PROSITE; PS00020; ACTININ 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 GTGTGCGATAAATTAAAGGTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding; Alternative splicing.
                                                                                                                                                                                                                                                                                                         Pfam, PF00681; Plectin, 5.
Pfam, PF00018; SH3; 1.
Pfam, PF00435; spectrin; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.75%
25.41%
7.04%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.61
EMBL, U04850; AAA57185.1;
PIR, 156317; A40937.
Genew, HGNC:1090; BPAGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  £; 5
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959
1077
1143
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3214
439
322
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                                                                                                                                                                                                                                                                                         Pfam; PF00307; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1670
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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DB:
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DOMAIN
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AATGCGGTCGCAAAACCATTCTAGGGCGTGGT~
                                                                                                                                                                                                (Rel. 40, Created)
                                                                                                                                                                                                                                                                (Penicillin G amidohydrolase)
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                 Bacillus megaterium.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 14945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1404;
                                                                                                                                                                              Q60<u>1</u>36; Q9S463;
16-OCT-2001 (Re)
                                                                                                                                                                                                                                                                                 PAC OR PGA.
                                                                                                                                                                                                                                                                                                                  Bacteria;
 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ThrMetGluLysValThrLysGluLys 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 AspAlaIleHisGlnGluLysIleGluThrLeuAlaSerLeuGluAsnSerArgGlnThr 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GluAlaLeuLysLeuAlaAla 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1036 LeuaspalaGluGlualaLeu-----LysalaAlaGlmLysLysAsnAspGluLeu 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400 GATGAATTATCCATAAAAACACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCGACT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATACGCAGAAAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGATTTTATGCGATGTGTGCGATAAATTAAAGGTC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITGGATTTGTTTGAGGTGCTTGTTTTTGGTAAAGACGGCGAAAAAAGACACAATGAAAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 AATTACAACAAGAAAACGACTTTAATTGAACAAAACAIGCTTTCTAAAATTTA 351
                                                                                                                                                                                                                                                                   Κĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 TIAACGCIGITIAAAAIGGGGGGITITIAAAICTIAICAAIIAGCIGICAII---GIIGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- AGAAGTTTGGAAGAAATGGATGATGAAGAAGTGAAAGAAATGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA
                                                                                                                  coil; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                       TOTALEHARIKELEOSILFEKTRADKLORELEDTR ->
ROISEDPEN (in isoform 3).
/FIId=VSP 000762.
s -> GGSSKVG (in isoform 3).
/FIId=VSP 000763.
T -> RRQISEDPENT (in isoform 4).
/FIId=VSP 000764.
K -> R (IN REF. 2; AAC03548).
E -> V (IN REF. 2; AAC03548).
                                                                                                                                                                                                                                                                                                                                                                                -> R (IN REF. 2; AAC03547).
-> V (IN REF. 2; AAC03548).
5631CB8683498E23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1433
52
36
74
51
                                                                                                                                                                                  SER-RICH.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (in isoform 2).
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Mismatches:
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               InterProj IPRO1038; CAP-GJy.
InterProj IPRO1038; CAP-GJy.
InterProj IPRO1078; CAP-GJy.
Pfam, PF01302; CAP-GLY, Z.
SMART; SM00343; ZNF C2HC; 1.
PROSITE; PS00845; CAP-GJY 2; 2.
Cytoskeleton; Microtubule; Colled
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                                                         AshValLysLeuAlaGluGluLeuGlyArgSerArgAspGluValThrSerHisGlnLys 1189
549
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Pfam; PF01804; Penicil amidase; 1.

Hydrolase; Antibiotic resistance; Zymogen; Calcium-binding; Signal.

SIGNAL 1 24 POTENTIAL.

PROTENTIAL. 25 802 PENICILLIN G ACYLASE ZYMOGEN.

CHAIN 25 234 PENICILLIN G ACYLASE ALPHA SUBJNIT.

PROPEP 235 265 SPACER PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Penicillin G acylase precursor (BC 3.5.1.11) (Penicillin G amidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Martin L.M., Prieto A.M., Cortes E., Garcia J.L.; "Cloning and sequencing of the pac gene encoding the penicillin G acylase of Bacillus megaterium ATCC 14945."; FEMS Microbiol. Lett. 125:287-292(1995).
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-!- COFACTOR: Binds 1 calcium ion per subunit (Potential).
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim Y.C.;
ne from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kang J.H., Kim S.J., Park Y.C., Hwang Y., Yoo O.J., Kim Nucleotide sequence of the penicillin G acylase gene fro Bacillus megaterium and characteristics of the enzyme."; Misainmurhag foiji 32:215-221 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                  1190 LeuglugludrgSerValLeuAsndSnGlnLeuLeu 1202
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--- SUBCELLULAR LOCATION: Extracellular (Potential).
--- SIMILARITY: Belongs to peptidase family 845.
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STRAIN=ATCC 14945;
MEDLINE=95180705; PubMed=7875576;
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EMBL; Z37542; CAA85774.1; -...
EMBL; AF161113; AAD45609.1; -...
PIR; S49252; S49252.
HSSP; P06875; 1AJQ.
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187 GAAGAGTTGCAATACTATGGGAGCAATAGTTTTGGGAGTTTCATTAAAGGCGAAGGAGTC 246
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169 ThrTyrPheMetAspAsnHisGlnGluLeuLysAsnAlaGlulleLeuAlaLysLeuGlu 188
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PENICILLIN G ACYLASE BETA SUBUNIT.
SY SIMILARITY.
CALCIUM (POTENTIAL).
CALCIUM (POTENTIAL).
                                               T -> M (IN STRAIN CA4098).

D -> E (IN STRAIN CA4098).

I -> K (IN STRAIN CA4098).

T -> S (IN STRAIN CA4098).

A -> T (IN STRAIN CA4098).

S -> M (IN STRAIN CA4098).

F -> Y (IN STRAIN CA4098).

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268	591	283	649	302		
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Search completed: July 5, 2004, 03:06:43 Job time: 20.5 secs

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08adwl bacteriopha
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08pic9 campylobact
09pie9 campylobact
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09rag9 oryza sativ
081329 borrelia bu
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Q88210 pseudomonas
Q8ijz2 plasmodium
O43633 homo sapien
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Q8rh57 fusobacteri
Q9zi88 borrelia bu
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Enterobacteriaceae, Salmonella.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MNS-2003 (TrEMBLrel. 24, Last annocation update)
Hypothetical protein (Positive regulator for sigma H (Sigma 32)
promoters, permitting growth at high temperature).
                    Q8flc7
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                     463 ACGCTGTTTAAA---ATGCGGGGTTTTAAATCTTATCAATTAGCTGTCATTGCTGCGAAT
                                                                                           160 SerieuAlaLysGlyValSerHisLeuLeuSerThrGlnLeuThrArgileLeuArgThr
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin Q., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Wa D., Qiang B., Wen Y., Hou Y.,
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SETAIN=24577 (ATCC 700930 / Serctype 2a;

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"Complete genome sequence and comparative genomics of Shigella T flexari serctype 2a Strain 2457T.";

Infect: Immun. 71:275-2786(2003).

EMBL; AR015039; AAN416571;

REMBL; AR015039; AAN416571;

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              SPECIES=S.Typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Sgetth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Floraca L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
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NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
NEDLINE-2153947; Pubmed=11677608;
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Baroks K., Chillingworth T., Connerton P., Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Cyail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella
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      SEQUENCE FROM N.A.
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ThrTrpLysNetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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                                                                           45 ArgAsnGluLeuPheLysSerMetGluGlyHisProGluGlnHisArgArgAsnTrpGln
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
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ThrTrpLysLysMetAspGluGluHisLysGlnGluPheLeuHisAlaValAspAlaArg 144
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|TyrLeuAsnAspSerAspLeuAspPheLeuGlnHisCysSerGluGluGlnLeuAlaAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ArgileLeuArgThrHisAlaAlaMetSerValLeuGlyHisGlyLeu---LeuArgGly
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
BMBL, AB016755; AAN78816.1;
InterPro; IPR005367; UPF0174.
Ffam, PF03667; UPF0114.
BHYPOCHELICAL BY CHOMPLE BRC190712375831D CRC64;
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Matches:
Conservative:
Mismatches:
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STRAIN=26695 / ATCC 703392;

STRAIN=26695 / ATCC 703392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kertchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Rleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Eee N., Adams M.D., Hickey B.K., McKenney K., RitzGerald L.M., Eee N., Peterson J.D., Kelley J.M., Berg D.E., Gocayne J.D., Viterback T.R., Peterson J.D., Kelley J.M., Footpan M.D., Weidman J.M., Fujiž C., Bowman C., Watthey L., Wallin E., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the gastric pathogen Helicobacter
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Enterobacteriaceae, Escherichia.
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
KRDILNB=21074935; PubMed=11205551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.
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01-MAR-2002 (TremBirel. 20, Last sequence update)
01-UTN-2003 (TremBirel. 24, Last annotation update)
Positive regulator for sigma 32 heat shock promoters.
HTGA OR Z0012 OR ECS0011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE53CF01F4C1C909 CRC64;
                                                           01-JAN-1998 (TrEVBLrel. 05, Created)
01-JAN-1998 (TrEVBLrel. 05, Last sequence update)
01-JUN-2003 (TrEVBLrel. 24, Last annotation update)
HP1590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pylori.";
Nature 388:539-547(1997).
EMBL; AE000565; AAD08629.1;
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MEDLINB=2115-211, PubMed=11258796;
MEDLINB=2115-211, PubMed=11258796;
MEDLINB=2115-211, PubMed=11258796;
MIN C.-G., Ohtsubo R., Nakayama K., Mirata T., Tanaka M., Tobe T.,
Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shinba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
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Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533 (2001).
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Seeger K., Murphy L., Harris D., Berriman M., Pain A., F
Seeger M., Murphy L., Harris D., Berriman M., Pain A., F
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL844507, CAD51332.1;
Hypothetical protein 1245 AA; 147911 MW; D856486AFDFE4DDF CRC64;
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AsnSerSerLeuArgIleSerThrLeuGluArgArgValLeuProPheSerLeuTrpVal 182
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                                               ACAAGCACCTCAAACAAATCCAATAAATCACTAGATTCCAATTGCTTTAAAAATTCCAAG
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-----LeuSerPhelleSerSerGlySerSerSer
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SERAIN=24577 / ATC7 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Rau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blatner F.R.;

"Complete genome sequence and comparative genomics of Shigella
Infect. Immun. 71:2772-2786(2003).

EMBL; AB016978; AAP15558.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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01-OCT-2003 (TrEMBirel. 25, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Positive regulator for sigma 32 heat shock promoters.
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Db 145 IleSerAspPheLeuLysGluAsnPheAsnIleGluLeuSerProGluValIleGluArg 164  Qy 331 AACATGCTITCTAAAATCTTAGAAAGAAGTTTGGAAGAATGGATGATGAAGAAGTG 387  :::::     :::    :::    :::      Db 165 HisTleLysLeuAlaLysValLysAspLeuAspLysProPheLeuGlnAspLeuAsnGln 184  Qy 388 AAAGAAATGTGCGATGATTATCCATAAAAACACGGACAATTTA 432  Db 185 LysAspPhAAlaGuGluAshValGLnLysAshCysThrSerGlnLeuLysIle 204	433 AACAGCATAAGCGGGGG	Db 225 PheAspValLysGlnGluPheValPhePheLysAsnGluGlyLysFroVal 241  Qy 502 GCTGTCATTGCGAATGGGGTGGGTGGCTTCTAGGGGGTGGTTTATGGCTTGGG 561	Qy 562 GGCAATCAGGTGCTTACAAGAACTCTGAGCTTTTTAACAGGTCCTGTTGGCTGGTT 62.	Oy 622 ACAGGCGTATGGACATTGATATTGCAGGGCCGGCTTATAGGGTAACCATACCGGCA 681	Qy 682 TGCATT	Oy 700 TTA	Qy         721 GCCAATGGAGATAAGAAGTCGTTGCAAATAGAATCCATT         759	SULT 9  DIMA PRELIMINARY; PRT; 276 AA.  QBDIMA; O1-MAR-2003 (TrEMBLrel. 23, Created)  O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)  O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)  Tlls[4] Protein.		[1] SEQUENCE FROM N.A. STRAIN=BP-1, MEDLINE=2225144, PubMed=12240834;	Nakamura I., Kaneko I., Sato S., Ikeuchi M., Ka Watanek A., Iriguchi M., Kawashima K., Kimura Kiyokawa C., Kobara M., Matsumoto M., Matsunot Shimpo S., Sugimoto M., Takeuchi C., Yamada M.,	RT "Complete genome structure of the thermophilic cyanobacterium RT Thermosynechococcus elongatus BP-1."; RL DNA Res. 9:123-130(2002). DR EMBLA AP005574; BAC09166.1;	COMPLETE PLOTEOME. SEQUENCE 276 AA; 31282 MW; D0577A9D97E0CA92 C ignment Scores:	Pred. No.: 6.11 Length: 276 Score: 102.50 Marches: 50 Percent Similarity: 39.16% Conservative: 53
	RESULT 8 QBR924  AC QBR924, PRELIMINARY; FRT; 403 AA. AC QBR924; DT 01-070X-2002 (TrEMBLrel. 21, Created) DT 01-070X-2003 (TrEMBLrel. 24, Last sequence update) DT 01-070X-2003 (TrEMBLrel. 24, Last amnotation update)	US HYPOCHETICAL protein TTE1436.  GN TTE1436.  OS Thermoanaerobacter tengcongensis.  OC Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales;  OC Thermoanaerobacteriaceae; Thermoanaerobacter.	RN [1] RP SEQUENCE FROM N.A. RC STRAIN=MB4 / JCM 11007; RX MFNT.NR=J1902616. Buhwad.11007326.	Bao O., Tian Y., Li W., Xu Z., Xuan Z., Hu S., D Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X Tan H., Chen R., Wang J., Yu J., Yang H.;	XI "A complete sequence of T. tengcongensis genome."; Genome Res. 12:689-700(2002). DR EMBL; ARO13102; AAM246581 DR GO:0009454; C:flagellar hook (sensu Bacteria); IEA.	GO; GC:0003774; GO; GC:0009296; InterPro; IPR001 Pfam; Pf02120; I	Hypoth	Alignment Scores:  Pred. No.:  103.50  Macches: 5.08  Macches: 63  Score: 103.50  Macches: 63  Score: 35.14\$  Conservative: 47  Best Local Similarity: 20.13\$  Query Match: 16  Mismatches: 98  T.67\$  Indels: 105  US-09-732-091-3 (1-759) x Q8R9Z4 (1-403)	Oy 28 GAATTTTAAAGCAATTGGAATCTAGTGATTTATTGGATTTTGTTTG	Cy         88         GGTAAAGACGCGAAAAAGACACAATGAAAAA	Qy 121TGACCAGCTCCATAGAATACAAAAGGGAT 150 :::       :::    ::::::::::::::::::::	Qy 151 GGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGGAGC 210 Db 113 AlaSerAspPheGluLysValArgGluLysLeuGluValAlalaLeuGln 128	Qy 211 AATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGACATTTTATGCGAT 270	Qy 271 GTGTGCGAFAAATTAAAGGTCAATTACAACAAGAAAACTGAAAGGACTTTAATTGAAGAA 330 :::

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                                                                                                                                                                                                                                                                                                                          94 GACGGCGAAAAAGACACAAT----GAAAAACTGACCAGCTCCATAGAATACAAAAGG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 GCCTTAAGCGCGGCGACTTTAACGCTGTTTAAATGGGGGGTTTTAAATCTTATCAATTA 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 CATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGG
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Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
                                                                                                                                                                                                                                     24 LeuGluLeuAlaThrGluGluGluLeuGlnAspLeuThrGluIleLeuFhe---
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| ProlleSerMetGluMetValArgLeuValLeuGluGlyGly----
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNA polymerase II largest subunit (Fragment).
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Mismatches:
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                                                                                                                           US-09-732-091-3 (1-759) x Q8DIH4 (1-276)
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                                                 RA Packs J.B., Marinets A., Ford Doolittle W., Cavalier-Smith T.,
RA Logsdon J.M. Jr.;
RA Logsdon J.M. Jr.;
Radlyses of RNA Polymerase II Genes from Free-Living Protists:
RT "Analyses of RNA Polymerase II Genes from Free-Living Protists:
RT Phylogeny, Long Branch Attraction, and the Bukaryotic Big Bang.";
RL Bhylogeny, Long Branch Attraction, and the Bukaryotic Big Bang.";
ROI. Biol. Bvol. 19:830-840(2002).
REMEL, AR9510; ARM451511.;
ROJ. GO:0005665; C:NNA-directed RNA polymerase II, core complex; IEA.
GO; GO:0005665; C:NNA-directed RNA polymerase activity; IEA.
GO; GO:0006366; P:transcription from Pol II promoter; IEA.
GO; GO:0006366; P:transcription, IEA.
GO; GO:0006366; P:transcription, IEA.
GO; GO:0006366; P:transcription, IEA.
ROJ. GO:0006366; P:transcription, IEA.
ROJ. GO:0006366; RNA pol Rpbl. 3.
RITERPRO; IPR007032; RNA pol Rpbl. 4.
RITERPRO; IPR007031; RNA pol Rpbl. 4.
RITERPRO; IPR007031; RNA pol Rpbl. 5.
RITERPRO; IPR007031; RNA pol Rpbl. 5.
RITERPRO; IPR007031; RNA pol Rpbl. 7.
REAM; PF04993; RNA pol Rpbl. 7.
REAM; PF04993; RNA pol Rpbl. 4; I.
REAM; PF04999; RNA pol Rpbl. 6; I.
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SEQUENCE FROM N.A.
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--GluLeuArgAsn 347
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368 HigGluTyrGluLysGlnAsnGluGluLeuArgAsnGluLysGluLysLeuGlnSerThr 387
                                                                                                                                                                                                                                                                                                                                                             193 TIGCAATACTAIGGGAGCAATAGTITIGCGAGTITCATTAAAGGCGAAGGAGTCTTATAC 252
                                                                                                                                                                                                                                                                                                                                                                                        364 GAAGAAATGGATGAAGAAGTGAAGAAATGTGCGATGAATTATCCATAAAAACACG 423
                                                                                   76 GTGCTTGTTTTTGGTAAAGACGGCGAAAAAGACACAATGAAAAACTGACCAGCTCCATA
                                                                                                                                                                                                                                                                     AAAGAGATTTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC-------AAG
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MEDILINE-$9262176; PubMed=10329464;
Balmisano A.N., Winton J.R., Dickhoff W.W.;
"Sequence features and phylogenetic analysis of the stress protein hsp90alpha in chinook salmon (Oncorhynchus tshawytscha), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Schlinopterygii, Neopterygii, Taleostel, Buteleostei,
Proteachthopterygii, Salmoniformes; Salmonidae, Oncorhynchus.
NCBI_TaxID-74940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oncorhynchus tschawytscha (Chinook salmon) (King salmon)
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61
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Biochem. Biophys. Res. Commun. 258:784-791(1999)
EMBL; U89945; AAB49983.1;
HSSP; P07900; 1BYQ.
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                                                                                                                333 GluArgGluLeuTyrTyrLeuGlyMetIleGlu-
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GO; GO: D003754; F: Chaperone activity; IEA.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
Pfam; PF02518; HATPase c; 1.
Pfam; PF00183; HSP90; 1.
                                        US-09-732-091-3 (1-759) x QBIKG8 (1-1455)
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SMART, SM00387; HATPase c; 1.
PROSITE, PS00298; HSP90; 1.
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MEDLINE=2255705; PubMed=12368864;

Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,

Gardnen J.A., Reland K.E., Bowman S., Paulsen I.T., James K.,

Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,

Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

Worfer J.C., Canucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                              400 GATGAATTA---TCCATAAAAACACGGACAATTTAAACAGACAAGCCTTAAGCGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CAAAACHIGCITITCIAAAAICITAGAAAGAAGITITGGAAGAAIGGAI-
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36FAA1760A898F99 CRC64;
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
PP14_0637.
                                                                                                                                                                                                                                                                                                                  980 Thrieu---LeuPheSerMet------
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                               Helicobacter
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Hypothetical
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GluAspGluAspGluLysLysLysGlnGluGluGluLeuAsnThrLys---PheGluAsnLeu
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AspaspTyrLysArgHisLysGluAsnLeuGluLysMetIleGluLysGlyLysAsnAsn 218
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                                                                                                                                                                                                                 M EQUENCE FROM N.A.

RX STRAINARCC 51449 / 3B1;

RX MEDLINE=2709201; PubMed=12810954;

RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., RA Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A., RA Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.,

RA Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.,

RT The complete genome sequence of the carcinogenic bacterium

RT Helicobacter hepaticus.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).

RML; AB017147; AAP77543.1;

RM Hypothetical protein; Complete proteome.
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LeuAlaAsnGlyValIleTrpGluValLysAspMetPheGluGlySerIleAspThrGlu 303
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| CysAscArgLeuMetCysGluAsnProArgIleThrAlaValAlaThrGlnSerIleVal
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                                                                                                                      Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
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Last annotation update)
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435 240 263

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146 AspLeuGlnLysLeu-----AsnAlaPheAlaArgSerAspGluGlySerAlaSerGln 163
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                               ----GICTTATACAAGAGATTTTTATGCGATGTGTGCGAT
                                                             164 ArgAspAlaIleValGlnAlaMetThrLeuPheGlnLysMetArgPheAspLeu----
                                                                                             280 AAATTAAAGGTCAATTACAACAAGAAAACTGAAAACGACTTTAATTGAACAAAACATGCTT
                                                                                                                           ---ArgGlyTyrThrTyrSerLeuLysAlaGluAsnArgAlaProAlaGluAlaSerMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGAAATGTGCGATGAATTA---TCCATAAAAAACACGGACAAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                      436 AGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGT
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EMBL, AR014829, AAN35246.1; -.
Hypothetical protein.
SEQUENCE 202 AA; 24259 MW; 48FD22A7F21165A6 CRC64;
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Last sequence update)
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PF10_0048.
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GluLeuLeuGlyIleIleLeuLysSerLeuPheSerAlaAlaTrpValValSerThrLeu 402
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                                                                                                                                                                                                                                                                                                                                                             Buell R., Joandar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., White C., Fraser C., Collmer A.; "Complete sequence of Pseudomonas syringae."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ARD16865; AROS6120.1; -.
                                                                                                                                                                                                                                                                         Gammaproteobacteria; Pseudomonadales;
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Last annotation update)
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Matches:
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Indels:
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GG; GO:0004801; F:signal transducer activity;
GG; GO:0006935; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; C:mtaxis_transd.
InterPro; IPR004089; C:mtaxis_transd.
InterPro; IPR00566; HAMP.
Pfont PF00672; HAMP; 1.
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50885; HAMP; 1.
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01-JUN-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Methyl-accepting chemotaxis protein.
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                                                                                                                                               PRT;
                                                                                                                                                                                                                                                          Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria; Gammaprot
Pseudomonadaceae; Pseudomonas.
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99.50
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403 AlaLeuGlu 405
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633 AA;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                         STRAIN=DC3000;
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Length: Matches: Conservative: Mismatches: Indels: Gaps:		GGAATTTTAAAGCAATTGGA	: elleLeuLeuLysLysLeuMet	TTTGAGGTGCTTGTTTTTGGTAAAGACGGCGAAAAAAAAGACAAT	AspGlnLysTyri	CAGCICCATAGAATACAAAAGG		TACGCBGAAAGAATC	:::::     :::      AsnPheLeuThrPheLeuLysGlySerPheGluLysValAlaGluGluIleGlnIle-	SAGTITCATTAAAGGCGAAGG	 	TGCGATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAA		ACGACT	PheGluSerGlnLeuAsnAla	TCTAAAATCTTAGAAAGAAGTTTGGAAGAAATGGATGAAGAAGTGAAA-	:::	GAAATGTGC	::::::    sperangemetLysIleCys	ž	11	
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Search completed: July 5, 2004, 03:06:06 Job time: 87.5 secs

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-LOOPEXT=0 -UNITG=bits -START=1 -Enb=-1 -HATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -AliGN=1S
-USER=UCGAL -OUTFNT=pcc -NORM=ext -HEAPSIZE=500 -MINEN=0 -MAXLEN=200000000
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-NO MAMP -LARGEQUERY -NEG SCORES=0 -WAIT -SSPENCOK=100 -XGAPEXT=0.5 -FGAPOP=6
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-489-039A-8852

US-09-543-681A-6437

US-08-658-639-12

US-08-944-604-12

US-08-134-0C1C-5279

US-09-134-0C1C-5279

US-09-919-172-29

US-09-543-681A-7696

US-09-328-352-5845
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No.
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERRENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
RIOR FILING DATE: 1998-07-27
SEQ ID NO 29941
LENGTH: 273
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Matches:
Conservative:
Mismatches:
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Sequence 29841, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-29841
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Sequence 8652, Application US/09489039A

Fatent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Cary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREDMONDAR FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REPRESENCE: 2709, 2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8852

LENGTH: 258
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                                                                                                                   TTAITGGAITIGITITGAGGIGCITGTITTTGGIAAAGACGGGAAAAAAGACACAATGAA 117
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                                                                           235 GGCGAAGGAGTCTTAIACAAAGAGAITITTAIGCGAIGTGGTGCGAIAAATTAAAGGTCAAI
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASRCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASRCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29840
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                                                                                                                                                    GAIGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTGAAACGACTTTAATTGAA 327
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|LeuAsnGlySerAlaLeuSerGly-----LeuValValProAlaValAlaArgMetIle 179
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                   TrpHisProGluHisArgArgTyrAlaSerAlaIleLeuAspGluLeuArgLeuPheGly
                                                                .48 CATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATGGG
                                                                                                                                                                                                                             102 AspvalAlaGlyLysLeuLysValLysGlyValGlySerMetGluLeulleGluLeuglu
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GGTAAAGACGGCGAAAAAAAGACACAATGAAAAACTGACCAGCTCCATAGAATACAAAAGG
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684 SerLysLysLeuThrAlaValLeuAspIleIle-GlnLysLeuMetAspLysIleMetG1 703
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Matches:
Conservative:
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Patent No. 5914238
GENERAL INFORMATION:
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APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
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APPLICANT: GRAY BRETON
APPLICANT: GRAY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                   TIGITIGAGGIGCITGITITIGGIAAAGACGCGAAAAAAGACACAAIGAAAAAACTGACC 126
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|SerTrpAsnLysteuAsnAlaGluGInLysAlaGlnPheLeuAlaAlaAlaValGluCysArg 153
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154 SerHisGluLeuAspSerLeuMetAlaHisLeuLeuArgHisArgLysLeuSerGluGly 173
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Best Local Similarity:
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US-09-543-681A-6437
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; Sequence 12, Application US/08944604
; Patent No. 6218131
; GENERAL INFORMATION:
APPLICANT: KERSEE, SUSAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATERIALS AND METHODS FOR DETECTION OF BREAST CANCER
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,98
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
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TITLE OF INVENTION: MATERIALS AND METHODS TITLE OF INVENTICM: BREAST CANCER NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADSRESSE: ADSRED: USA
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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43.58%
22.91%
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Best Local Similarity:
Query Match:
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146 GGCATGGCGATGATTACGCTAAATACGCAGAAAGAATCGCTGAAGAGTTGCAATACTATG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 IGGGGGGTITIAAAICITAATCAATTAGCTGICAITGTIGCGAAIGCGGICGCA 528
                                                                                               APPLICANT: GBAR, ROBERT
APPLICANT: WIN YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/94,604
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: MTP-021 (8395/24)
TELECOMMINICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 173 amino acids
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Matches:
Conservative:
Mismatches:
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Gaps:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5279
                                                                                                                                                          GIGCITGITITIGGIAAA---GACGGCGAAAAAGACACAAIGAAAAGIGAAAAACTGACCAGCTCC 132
                                                                                                                                                                                                                                                     110 MetGlyThrMetAsnArgGlnLeuLysLeuProGlnIleGlnLysIleMetMetGluPhe 129
                                                                                                                                                                                                                                                                                                                                                                                            170 GluLeuGlyLeuSerLeuThrAspGluLeuSerAsnLeuProSerThrGlyGlySerLeu 189
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                                                                                                                                                                                                                                                                                                    238 GAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTAC 297
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                                                                                                                                                                                               70 ArgArgTyrValArgLysPheValLeuMetArgAlaAsnIleGlnAlaValSerLeuLys 83
                                             193 TTGCAATACTATGGGAGC---AATAGTTTTGCGAGTTTCATTAAAGGC
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Mismatches:
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Matches:
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; Patent No. 6380370
; GENERAL INFORMATION:
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Query Match:
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; ORGANISM: Staphy
US-09-134-001C-5279
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                                251 ACAAAGAGATITITATGCGATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTG 310
                                                                                                     416 AAAACACGGACAATTTAAACAGACAAGCCTTAAGCGGGGGGGCGTTTTAACGCTGTTTAAAA 475
                                                        snargdlnieulysLeuProGlnIleGlnLysIleMetMetGluPheGluArgGlnAlaG 85
ysSerAsnAsnSerMetAlaGlnAlaMetLysGlyValThrLysAlaMetGlyThrMetA 65
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105 luGluAspGluGluGluSerAspAlaValValSerGlnValLeuAspGluLeuGlyLeuS
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APPLICANT: OBAR, ROBERT
APPLICANT: WJ, YING-JYE
APPLICANT: WJ, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BREAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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339
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MEYERS, THOWAS C
REGISTATION NUMBER: 36,989
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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47.80%
21.43%
7.34%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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FILING DATE:
CLASSIFICATION: 435
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-08-944-604-16
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Sequence 7696, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION UNMERR: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-09
PRIOR APPLICATION UNMERR: US 60/128,706
PRIOR APPLICATION UNMERR: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
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1086 ArgCysGluhlaLeuLysIleGlnAlaAspGlyPheLysAspGlnLeuArgSerThrAsn 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1123 LysCysLeuGluGluAspLeuAlaLysSerGlnAsnLeuValSerGluPheLysGlnLys 1142
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|1143 CysAspGlnGlnAsnIleIleIleGlnAsnThrLysLy9GluValArgAsnLeuAsnAla 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                               166 AAATACGCAGAAAGAATCGCTGAAGAGTTG-----CAATACTATGGGAGCAATAGTTTT 219
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                                                                                                                                                                                                                                                                                                                                                           106 AGACACATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCT
                                                                     2125
46
35
62
38
     INFORMATION: Incyte ID No. 6673545 3774181CD1
                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                     95.00
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25.41%
7.04%
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US-09-543-681A-7696
                                                                                                  Percent Similarity:
Best Local Similarity:
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1163 Glu 1163
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US-09-543-681A-7696
                                                Alignment Scores:
Pred. No.:
        TS-09-919-172-29
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209 HisAlaPhe-----ValProSerGlyAspLeuAlaThrIleIleIleAlaAlaVal 225
                                                                                                                                                         .::|||
28 ThrSerArgGluAlaLeulleLysAspValValMetIleAlaAlaArgIleLeuLeuGlu 47
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                                                                                                                                                                                                                                                                                             68 TyrProGluSerAsnSerPheValThrAsnThrVallleGluPheValLeuHisAsnGlu 87
TACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTATTGGAT
                                                                                       199 TACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAG
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| Patent No. 6673545
| GANERAL INFORMATION:
| APPLICANT: Faris, Mary
| APPLICANT: Turner, Christopher M.
| ITTLE OF INVENTION: PROSTATE CANCER MARKERS
| FILE REPERENCE: PA-036 US
| CURRENT APPLICATION NUMBER: US/09/919,172
| CURRENT FILING DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: 60/222,469
| PRIOR APPLICATION NUMBER: 60/222,469
| PRIOR APPLICATION NUMBER: 500-07-28
| NUMBER OF SEQ ID NOS: 102
| SEQ ID NO 29
| LENGTH: 2125
                   127 AGCTCC-----
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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Sequence 5845, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 GATGATGAAGAAGTGAAAGAAATGTGCGATGAATTATCCATAAAAAACACGGACAATTTA 432
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146 AsnGlyGluGlnLeuValGluLeu------ValLeuAspAlaSerSer 160
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                                                                                                                                                                                                                                                                                                                                                                                      -----GGGAGCAATAGTTTTGCG-----AGTTTCATTAAAGGCGAAGGAGTCTTATAC 252
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|GlnAspLeuSerValLysPheSerSerPheValAspAlaThrGlnMetAlaGluAlaAla 136
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Mismatches:
Indels:
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Matches:
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                   ; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-749
                                                                                         89.50
41.18%
21.96%
6.63%
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Batent No. 6559294

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering the RILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

VURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                     187 GAAGAGTIGCAATACTATGGGAGCAATAGTTTTGCGAGTTTTCATTAAAGGCGAAGGAG
                                                                                                                                                                                                                                                                                                                                                     --- LeuArgGlnIleAspval
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443
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PhealaTyrAspargGlyLysGlu---ileGluGlmMetGln--
             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                           91.50
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US-09-138-452A-749
Alignment Scores:
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and Methods for Control of Invertebrates
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11831 ProGluAsnLeuAsnAspIleIleThrAspGlnLeuArgAspPheMetAlaGlnGluLeu 262
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ValAspTyrAsnGlnValValLeuHisIleLeuAspAsnTyrAspGlnArgLeuGluGlu 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                173 ValSerArgAsnSerLeuAsnPheAspMetAlaSerGluValGlnSerThrAspAlaAla
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                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 PheGlyAlaAlaProSerGlySerGlyThr-----
   TITLE OF INVENTION: Compositions, and Meth
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: US/09/345,236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: ZastSEQ for Windows Version 3.0
SEQ ID NO 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 CITGCGGCAAICAGGIG-----
                                                                                                                              TYPE: PRT ORGANISM: mosquito baculovirus
                                                                                                                                                                                                           0.106
89.50
36.86%
23.53%
6.63%
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Best Local Similarity:
Query Match:
DB:
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GluTyrProValValSerGlyValPhe-----LysLeuLeuCysAspThrAlaGlnSer 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCATAAAAACACGGACAATTTAAACAGACAAGGCCTTAAGCGCGGGGGGACTTTAACGCTG 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 AGITICATIAAAGGCGAAGGAGICTIAIACAAAGAGAITITAIGCGAI----
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REPRENEUR: GT039-032A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/09345236B
Patent No. 6521454
GENERAL INPORMATION:
APPLICANT: Tuknor, Bettina
APPLICANT: Moser, Bettina
APPLICANT: Moser, Bettina
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543
31
52
67
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                         ) ORGANISM: Acinetobacter baumannii
US-09-328-352-5845
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89.50
37.37%
21.05%
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US-09-345-236B-98
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323 LeuleuSerpheArgThrLysThr-----TyrilelleAlaGluGlyValProHisAsp 340
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303 ValAspTyrAsnGlnValValLeuHisIleLeuAspAsnTyrAspGlnArgLeuGluGlu 322
                                                                                                                               Sequence 50, Application US/09446301A
Patent No. 6506893
GENERAL INFORMATION:
APPLICANT: BL.SOLH, NEVINE
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
TITLE OF INVENTION: COMPOUNDS
GURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT PALICATION NUMBER: US/09/446,301A
SOURMER OF SEQ ID NOS: 51
SOURMER PATENTING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
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                                                                                                        622 ACAGGCGIATGGACAGCGALTGAIATTGCAGGCCCGGCTTALAGGGTAACCATACCGGCA
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                                     ACTOTGAGOTITITAACAGGTCCTGTTGGCTGGATCATT
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Mismatches:
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ORGANISM: Staphylococcus sp.
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46.58%
25.34%
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LENGIH: 560
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                                 Sequence 121, Application US/09345236B

Petent No. 6521454

GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Mescr. Jettina
APPLICANT: Mescr. Jettina
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: White, Susan E.
APPLICANT: Occkburn, Andrew, Albert H.
APPLICANT: Occkburn, Compositions, and Methods for Control of Invertebrates
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
CURRENT FILE REPRESENCE: 21042.0004
CURRENT FILENG DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 121
EDECTH: 546
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ValPheGluValValGlyGlyGlyProGluGlyAspTyrAlaAlaGlyGluAspGlu 172
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| LysValMetGluLeuPheAsrAlaLeuSerGluGluGlnArgAsnValIleLeuAsnAsn 212
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283 AlaLeuAlaileThrValAlaAspArgValSerArgSerPheMetTyrGluGlyArgile 302
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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CRGANISM: mosquito baculovirus
US-09-345-2368-121
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Best Local Similarity:
                    US-09-345-236B-121
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Search completed: July 5, 2004, 03:07:23 Job time : 21.5 secs

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Sequence 9162, Ap
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Sequence 17, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 16, Appl
Sequence 43832, A
Sequence 191043,
Sequence 76490, A
Sequence 742, Appl
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 169, App
Sequence 220, App
Sequence 230, App
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Sequence 12141, A
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Sequence 1075, Ap
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Sequence 12254,
Sequence 530, App
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Sequence 14395, A
Sequence 54543, A
Sequence 29, Appl
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                                                                                                                                    Sequence 414, App
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APPLICANT: Tall Jung-Hui
APPLICANT: Tall Jung-Hui
APPLICANT: Tallker, Richard I.
APPLICANT: Jackson, W. James
IITILE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITILE OF INVENTION: Helicobacter proteins, gene sequences and uses
FILE REPERENCE: 7969-088
FULLE REPERENCE: 7969-088
FULLE REPERENCE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
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; Patent No. US20020107368A1
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-Q=/GG12 1/USFTO spool/USG9732091/runat 02072004 182407 19065/app_query.fasta 1.903
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-LOOPOL=0 -LCOPEXT=0 -UNITS=bits -STRAKT=1 -END=-1 -NATRL=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -THR NX*=100
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Mismatches:
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                                                             Length:
Matches:
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1279.00
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; SOFTWARE: Patentin Ver.; SEQ ID NO 44
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter spus-
                                                                                   Best Local Similarity:
                                                                           Percent Similarity
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                                                                                                                                               13
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RESULT 3
8-10-315-977-9162
8-10-315-977-9162
Sequence 9162 Application US/10335977
Publication No. US20040052799AI

gene sequences and uses

proteins,

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421 ACGGACAAITIAAACAGACAAGCCITAAGCGCGGCGACTITAACGCTGITTAAAATGGGG 480
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US-10-335-277-2463

US-10-335-277-2463

Sequence 9163, Application US/10335977

Sequence 9163, Application US/20335977

FUBICATION NO. US20040052799A1

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

DIAGNISTICS AND THERAPEUTICS

TOTAL COMMISSIONERS

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OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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TELEPRA: (617)42-4214
INFORMATION FOR SEQ ID NO: 9163:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
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              APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICCBACTER PYLORI
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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Indels:
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             ZIP: 02109-1875
COMPUTER READABLE FORM:
WEDTUM TYPE: CD/ROM ISO9660
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
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CCATION: (B) LOCATION 1...253

SECUENCE DESCRIPTION: SEQ ID NO: 9162:
US-10-335-977-9162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: (617)227-7400
(617)742-4214
                                                                                                                                                               ADDRESSEE: LAHIVE & COC
STREET: 28 State Street
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SEQUENCE CHARACTERISTICS;
                                                                                                                SEQUENCES: 10031
                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                         COUNTRY: USA
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GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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            RESULT 5
US_10_335_277-9164

i Sequence 9164
i Sequence 9164
i Publication No. U220040052799A1
i GENERAL INFORMATION:
i APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
i TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256
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Matches:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MANDERGOUTES, AMY B.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 9164:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 9164:
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                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
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1270.00
99.60%
99.21%
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TTGGATTTGTTTGAGGTGCTTGTTTTGGTAAAGACGGCGAAAAAAGACACAATGAAAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 ThrAspAsnLeuAsnArgGlnAlaLeuSerAlaAlaThrLeuThrLeuPheLysMetGly 160
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                                                                                                                                                                                                                                                                                                                                                                             2 ATGGCATACAAATATGATAGAGACTTGGAATTTTTAAAGCAATTGGAATCTAGTGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ILeAlaGluGluLeuGlnTyrTyrGlySerAsnSerPheAlaSerPheIleLysGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
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                                                                                                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                            US-09-732-091-3 (1-759) x US-10-335-977-9163 (1-253)
                                                                                                                                                                                                                                                                           Mismatches:
Indels:
Gaps:
                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...253
SEQUENCE DESCRIPTION: SEQ ID NO: 9163;
                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                          6.11e-122
1270.00
99.60%
99.21%
94.14%
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                    US-10-335-977-9163
                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
                                                                                                   FEATURE
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31 ValTyrAspGluAspGlyThrLeuArgMetAsnGluGluLeuThrSerLeuThrGluTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACAGACAAGCCTTAAGCGCGGCGACTTTAACGCTGTTTAAAATGGGGGGGTTTTAAATCT
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141
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36
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Matches:
Conservative:
Xismatches:
Indels:
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                                                                                                                                                      ORGANISM: Helicobacter pylori
                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...2
SEQUENCE DESCRIPTION: SEQ ID NO:
            (617)227-7400
                                                                   LENGTH: 248 amino acids
TYPE: amino acid
                      TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7699:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       1.9e-65
722.00
75.64%
60.26%
53.52%
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                          US-09-732-091-3 (1-759)
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                   64 ileAlaGiuGluieuGlnIyrIYrGIySerAsnSerPheAlaSerPheIleLysGlyGlu
ATCGCTGAAGAGTTGCAATACTATGGGAGCAATAGTTTTGCGAGTTTCATTAAAGGCGAA
                                                      GGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTCAATTACAAC
                                                                                                               aagaaaactgaaacgactttaattgaacaaaacatgctttctaaaatcttagaaagt
                                                                                                                                TTGGAAGAATGGATGATGAAGAAGTGAAAGAATGTGCGATGAATTATCCATAAAAAC
                                                                                                                                                                                           ACGGACAATTTAAACAGACAAGCCTTAAGCGCGGGGGGCTTTTAACGCTGTTTAAAATGGGG
                                                                                                                                                                                                                                                GGTTTTAAATCTTATCAATTAGCTGTCATTGTTGCGAATGCGGTCGCAAAAACCATTCTA
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10S-10-21S-977-7699
1 Sequence 7699, Application US/10335977
2 Publication No. US20040652799A1
3 GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
7 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
7 PLACED AND THERAPEUTICS
7 PLACED AND AMINO ACID SEQUENCES
7 PLACED AND AMINO ACID SEQUENCES
7 PLACED AND AMINO ACID SEQUENCES
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7 PLACED AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 AlaAsnGluAspLysLysSerLeuGlnIleGluSerVal 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 35,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROW ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: UNIX
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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Coomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
FILE REPRESENCE: 06132/047002
CURRENT APPLICATION NUMBER: US /09/882,227
CURRENT PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
RRICR APPLICATION NUMBER: US 08/902,615
RRICR APPLICATION NUMBER: US 08/902,615
RRICR FILING DATE: 1997-07-29
RNUMBER OF SEQ ID NOS: 638
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                  GAACAAAACATGCTTTCTAAAATCTTAGAAAGAAGTTTGGAAGAAATGGATGATGAAGAA 384
                                             61 GlyGlyAsnSerPheAlaAsnPhePheArgAspGluGlyValLeuTyrLysGluIleLeu
                                                                                             TGCGATGTGTGCGATAAATTAAAGGTCAATTACAACAAGAAAACTGAAACGGACTTTAATT
                                                                                                                                                                                             385 GTGAAAGAAATGTGCGATGAATTATCCATAAAAACACGGACAATTTA-----AAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r Sequence 414, Application US/09882227 Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.85e-40
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78.23$
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Best Local Similarity:
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                                                               Sequence 7698, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
ThrValProAlaCysValLeuValAlaThrLeuArgLysLys 244
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...237
SEQUENCE DESCRIPTION: SEQ ID NO: 7698;
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 237 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7698:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFEX: (617)742-4214
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10031
                                                                                                                                                                                                                                                                                         STATE: Massachusetts
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716.00
75.54*
60.09*
53.08*
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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                                                                                                                      Sequence 17, Application US/09732091
Patent No. US200201073681
GENERAL INFORMATION
APPLICANT: Tian, Jing-Hui
APPLICANT: Halker, Richard I.
APPLICANT: Halker, Richard I.
APPLICANT: Halker, Richard I.
APPLICANT: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
TITLE OF INVENTION: Helicobacter proteins, gene sequences and uses
CURRENT APPLICATION NUMBER: US/09/732,091
CURRENT APPLICATION NUMBER: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09732091
| Patent No. US20020107368A1
| GENERAL INFORMATION:
| APPLICANT: Tian, Jing-Hui
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| APPLICANT: Walker, Richard I.
| TITLE OF INVENTION: Helcobacter proteins, gene sequences and uses:
| TITLE OF INVENTION: Helcobacter proteins, gene sequences and uses:
| TITLE OF INVENTION: Helcobacter proteins, gene sequences and uses:
| TITLE OF INVENTION: Hereof
| FILE REPRENCE: 7969-088
| CURRENT APPLICATION NUMBER: US/09/732,091
| UNRENT FILING DATE: 2000-12-07
| SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 TTTGCGAGTTTCATTAAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGAT
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Mismatches:
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Matches:
Conservative:
Mismatches:
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         41 GlyAspLysLysSerLeuGlnIleGlu
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; TYPE: PRT
; ORGANISM: Helicobacter sp.
US-09-732-091-19
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ORGANISM: Helicobacter
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Best Local Similarity:
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Pred. No.:
                                                                      RESULT 10
US-09-732-091-17
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Pred. No.:
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US-09-732-091-19
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LENGTH: 38
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                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                    292 AATTACAACAAGAAAACTGAAACGACTITAATTGAACAAAACATGCTTTCTAAAATCTTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 LysAspSerLeuGluLysMetSerArgArgGlulleLysGluLeuCysAsnGluLeuGluLeuGluLysAsnGluLeuGluLeuGluLysAsnGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluLeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeuGluCeu
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AATGAAAAACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAATAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProArgAleAlaGluGluLeuGlnHisTyrGlyGlyAsnSerPheAlaAsnPhePhe 41
                                                                                                                                                                                                                                                                          42 ArgAspGluG1yValLeuTyrLysGlu11eLeuCysAspAlaCysAspHisLeuIysVal 61
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                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                    607 GTIGGCIGGATCATIACAGGCGIAIGGACAGCGATIGATAITGCAGGGCCGGCTIAIAGG 666
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                                   232 AAAGGCGAAGGAGTCTTATACAAAGAGATTTTATGCGATGTGTGCGATAAATTAAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09732091
Fatent No. US202020107368A1
GENERAL INFORMATION: Tian, Jing-Rui
APPLICANT: Tian, Jing-Rui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, R. James
ITILE OF INVENTION: Thereof
FILE REFERENCE: 7969-088
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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Mismatches:
Indels:
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ORGANISM: Helicobacter sp.
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GRERAL INCOMENTION:

APPLICANT: Wang, Liangsu

APPLICANT: Samudio, Carlos

APPLICANT: Samudio, Carlos

APPLICANT: Samudio, Carlos

APPLICANT: Asselbeck, Rari

APPLICANT: Carlos

APPLICANT: Carlos

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APPLICANT: Carlos

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APPLICANT: Carlos

APPLICANT: Trandck, John

APPLICANT: Trandck, John

APPLICANT: Trandck, John

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APPLICANT: Trandck, John

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

APPLICANT: Xu, Hasselbeck, Robert

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-66

PRIOR FILING DATE: 2000-01-22

PRIOR PILING DATE: 2000-01-22

PRIOR PILING DATE: 2000-01-22

PRIOR PILING DATE: 2000-01-22

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/250,305

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/250,305

PRIOR APPLICATION NUMBER: 60/250,306

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/250,306

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

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                                                                                                                                                                                                                                                                                                                                           21 LeuAspLeuPheGluValLeuValPheGly 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 43832, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                    21 TyrGinLeualaValileValhlaAsnAlaValAlatysThrileLeuGlyArgGlyLeu 40
Sequence 16, Application US/09732091
Sequence 16, Application US/09732091
Sequence 16, Application US/09732091
Sequence 16, Application.
Sequence 16, Application.
APPLICANT: Tan, Jing-Hui
APPLICANT: Tan, Jing-Hui
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
APPLICANT: Walker, Richard I.
TILLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TILLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TILLE OF INVENTION: Helicobacter proteins, gene sequences and uses;
TILLE OF INVENTION: 1969-088
CURRENT PALLICA DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 30
                                                                                                                                                                                                                                                                                          US-09-732-091-18

Sequence 18, Application US/09732091

Sequence 18, Application US/09732091

Sequence 18, Application US/09732091

Sexuence 18, Application US/09732091

SENERAL INFORMATION:

APPLICANT: Valker, Richard I.

APPLICANT: Walker, Richard I.

APPLICANT: Walker, Richard I.

APPLICANT: Jackson, W. James

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

CURRENT APPLICATION NUMBER: US/09/732,091

CURRENT FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Helicobacter sp.
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; ORGANISM: Helicobacter sp.
US-09-732-091-16
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Best Local Similarity:
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US-09-732-091-16
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Boukharov, Andrey A. Barbazuk, Brad

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                          TTAAAGCAATTGGAA
                                         TCTAGTGATTTATTGGATTTGAGGTGCTTGTTTTTGGTAAAGACGGCGAAAAAGA
                                                                                    109 CACANTGABABACTGACCAGCTCCATAGAATACAAAAGGCATGGCGATGATTACGCTAAA
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897 IleAspValPheAspLeuHisSerAsnLys-----SerArgHisIleSerSerLeuSer
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US-09-732-091-3 (1-759) x US-10-282-122A-43832 (1-1009)
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Sequence 191043, Application US/10437963
Publication No. US2040123343A1
SERNEAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated Witl
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 191043
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547 AspGluPheAsnGluMetGlnGluGlyLeuThrAsnLysLeuGlyGluValGluSerVal 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 TACAACAAGAAACTGAAACGACTTTAATTGAACAAACATGCTTTCTAAAATCTTAGAA 354
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617 -----GluSerThrSerGlnGluLeuValAspGluArgLysThrValThrLeuAsn 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 HisLysGlyGlnGluGluLeuGlu---AlaThrSerAsnGluLeuAlaSer1leValGlu
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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